

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:34:18 ; Search time 188 Seconds
(without alignments)
35.057 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYETKXNQSRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	15	ABR61469	ABR61469 Human dis
2	79	100.0	355	ADG89869	ADG89869 Human kin
3	79	100.0	355	ADV50412	ADV50412 Human CEN
4	79	100.0	496	ADG89867	ADG89867 Human kin
5	79	100.0	2503	ADW44257	ADW44257 Human cen
6	79	100.0	2543	ADW44255	ADW44255 Human cen
7	79	100.0	2568	ADW44253	ADW44253 Human cen
8	79	100.0	2633	ABG06505	ABG06505 Novel hum
9	79	100.0	2663	AAM39097	AAM39097 Human pol
10	79	100.0	2663	ADQ17932	ADQ17932 Human sof
11	79	100.0	2663	ADQ06867	ADQ06867 Cyclin-de
12	79	100.0	2688	AAM40883	AAM40883 Human pol
13	69	87.3	2954	AAY01632	AAY01632 Amino aci
14	65	82.3	694	ADX97061	ADX97061 Plant ful
15	64	68.4	955	AAR57365	AAR57365 K39 polyp
16	54	68.4	955	AAR03691	AAR03691 Leishmani
17	53	67.1	2013	ABE62322	ABE62322 Drosophil
18	52	65.8	154	AAB40661	AAB40661 Human ORF
19	52	65.8	154	ABP31636	ABP31636 Human str
20	52	65.8	341	ABB80079	ABB80079 Human kin
21	52	65.8	341	ABG72398	ABG72398 Human kin
22	52	65.8	348	ABR44339	ABR44339 Polypepti
23	52	65.8	1279	ABB80078	ABB80078 Human kin
24	52	65.8	1279	ABG70787	ABG70787 Human kin

25	52	65.8	1279	6	ABG72397	ABG72397 Human par
26	52	65.8	1401	7	ADJ94914	ADJ94914 Novel NOV
27	52	65.8	1931	4	ABB61012	ABB61012 Drosophil
28	51	64.6	829	3	AAG31117	AAG31117 Arabidops
29	51	64.6	829	3	AAG31117	AAG31117 Arabidops
30	51	64.6	834	3	AAG31116	AAG31116 Arabidops
31	50	63.3	677	4	ABB65183	ABB65183 Drosophil
32	49	62.0	172	3	AGL14279	AGL14279 Arabidops
33	49	62.0	346	7	ADC23342	ADC23342 Human kin
34	49	62.0	346	8	ADQ60232	ADQ60232 Human mic
35	49	62.0	346	8	ADQ88357	ADQ88357 Human kin
36	49	62.0	370	7	ADC23338	ADC23338 Human kin
37	49	62.0	370	8	ADQ60228	ADQ60228 Human mic
38	49	62.0	370	8	ADQ88353	ADQ88353 Human mic
39	49	62.0	460	3	AAB56650	AAB56650 Human pro
40	49	62.0	487	7	ADC23344	ADC23344 Human kin
41	49	62.0	487	8	ADQ60234	ADQ60234 Human mic
42	49	62.0	487	8	ADQ88359	ADQ88359 Human mic
43	49	62.0	490	7	ADK40973	ADK40973 Novel hum
44	49	62.0	490	8	ADR15692	ADR15692 Kinase 73
45	49	62.0	512	7	ADC23340	ADC23340 Human kin
46	49	62.0	512	8	ADQ60230	ADQ60230 Human mic
47	49	62.0	512	8	ADQ88355	ADQ88355 Human mic
48	49	62.0	665	8	ADQ09240	ADQ09240 Human KNS
49	49	62.0	665	8	ABM81748	ABM81748 Tumour-as
50	49	62.0	2033	9	ADZ13122	ADZ13122 Murine ca
51	48	60.8	324	2	AAW70235	AAW70235 Leishmani
52	48	60.8	324	5	AAE24949	AAE24949 Leishmani
53	48	60.8	324	5	AAU71831	AAU71831 Leishmani
54	48	60.8	324	5	ABG60887	ABG60887 Leishmani
55	48	60.8	324	5	ABG71285	ABG71285 L. chagas
56	48	60.8	324	7	ADB78816	ADB78816 Leishmani
57	47	59.5	54	5	ABB53101	ABB53101 Human ORP
58	47	59.5	458	8	ADX96421	ADX96421 Plant ful
59	47	59.5	670	8	ADN23314	ADN23314 Bacterial
60	47	59.5	754	8	ADN72187	ADN72187 Thale cre
61	46	58.2	398	3	AG21667	AG21667 Arabidops
62	46	58.2	452	3	AG21666	AG21666 Arabidops
63	46	58.2	469	3	AG21665	AG21665 Arabidops
64	46	58.2	922	8	ADM77741	ADM77741 A. thalia
65	46	58.2	938	8	ADT04834	ADT04834 Thale cre
66	46	58.2	955	8	ADM67694	ADM67694 Tobacco N
67	46	58.2	955	8	ADT04787	ADT04787 Common to
68	45	57.0	191	4	ABB15077	ABB15077 Human ner
69	45	57.0	201	4	ADM19729	ADM19729 Protein e
70	45	57.0	315	5	ABB47850	ABB47850 Listeria
71	45	57.0	328	8	ADX76282	ADX76282 Plant ful
72	45	57.0	352	9	ADV50410	ADV50410 Human uKH
73	45	57.0	355	9	ADV50411	ADV50411 Human NKH
74	45	57.0	384	4	ADM19736	ADM19736 Protein e
75	45	57.0	411	2	AAW72745	AAW72745 Drosophil
76	45	57.0	411	2	AAW72744	AAW72744 Drosophil
77	45	57.0	441	2	AAW72744	AAW72744 Drosophil
78	45	57.0	915	8	ADQ97735	ADQ97735 Human can
79	45	57.0	956	7	ADB67086	ADB67086 Kinesin h
80	45	57.0	956	8	ADQ97732	ADQ97732 Mouse can
81	45	57.0	956	9	ABE08337	ABE08337 c-Jun inh
82	45	57.0	957	7	ADB67085	ADB67085 Kinesin h
83	45	57.0	959	8	ADL99356	ADL99356 Nanostruc
84	45	57.0	959	8	ADL99357	ADL99357 Nanostruc
85	45	57.0	963	4	AAW78880	AAW78880 Human pro
86	45	57.0	963	7	ADB67089	ADB67089 Kinesin h
87	45	57.0	963	7	ADB67091	ADB67091 Kinesin h
88	45	57.0	963	9	ABE08391	ABE08391 c-Jun inh
89	45	57.0	964	8	ADL99362	ADL99362 Nanostruc
90	45	57.0	964	8	ADL99360	ADL99360 Nanostruc
91	45	57.0	967	7	ADB67090	ADB67090 Kinesin h
92	45	57.0	970	8	ADL99361	ADL99361 Nanostruc
93	45	57.0	975	2	AAW72746	AAW72746 Drosophil
94	45	57.0	975	4	ABE63485	ABE63485 Drosophil
95	45	57.0	975	7	ADB67088	ADB67088 Kinesin h
96	45	57.0	975	8	ADL99359	ADL99359 Nanostruc
97	45	57.0	979	4	AAW79864	AAW79864 Human pro

98	45	57.0	1011	6	ABR54195	Abv54195 Human NOV	171	40	50.6	205	5	AAE14609	Aae14609 Human mic
99	45	57.0	1011	7	ADK18370	Adk18370 Human NOV	172	40	50.6	205	6	ABU08213	Abu08213 Human kin
100	45	57.0	1027	7	ADB67096	Adb67096 Neuroal	173	40	50.6	205	6	ADA09079	Ada09079 Human gen
101	45	57.0	1027	8	ADL99367	Adl99367 Nanostruc	174	40	50.6	216	4	AAE03411	Aae03411 Human gen
102	45	57.0	1027	9	AEBO8355	Aeb08355 c-Jun inh	175	40	50.6	302	4	AGS93108	Agsg93108 C Glutami
103	45	57.0	1031	7	ADB67093	Adb67093 Kinesin h	176	40	50.6	401	7	ADM05302	Adm05302 Human pro
104	45	57.0	1032	7	ADB67093	Adb67093 Neuroal	177	40	50.6	784	4	ABB71112	Abb71112 Drosophil
105	45	57.0	1032	8	ADL99366	Adl99366 Nanostruc	178	40	50.6	814	8	ADQ67765	Adq67765 Novel hum
106	45	57.0	1032	8	ADL99366	Adl99366 Nanostruc	179	40	50.6	916	7	ADJ95102	Adj95102 Novel NOV
107	45	57.0	1269	3	AAV77955	Aay77955 A. thalia	180	40	50.6	1003	4	ABB61405	Abb61405 Drosophil
108	45	57.0	1269	3	AAV77955	Aay77955 A. thalia	181	40	50.6	1142	4	AGS70713	Agsg70713 S cerevis
109	44	55.7	348	4	ABU53208	Abu53208 Human cel	182	40	50.6	1142	6	ABR53123	Abv53123 Protein s
110	44	55.7	365	8	ADL73524	Adl73524 Plant ful	183	40	50.6	1142	7	ADK63074	Adk63074 Disease t
111	44	55.7	366	4	ABU53125	Abu53125 Intracell	184	40	50.6	1142	8	ADI26783	Adi26783 Saccharom
112	44	55.7	683	7	ABO77443	Abv77443 Pseudomon	185	40	50.6	1142	8	ADN19047	Adn19047 Bacterial
113	44	55.7	706	7	ADB67098	Adb67098 Kinesin-1	186	40	50.6	1226	8	ADQ36873	Adq36873 Cell prol
114	44	55.7	706	8	ADL99369	Adl99369 Nanostruc	187	39	49.4	225	2	AAW60574	Aaw60574 Human tra
115	44	55.7	706	8	ADL99369	Adl99369 Nanostruc	188	39	49.4	292	2	AAW60573	Aaw60573 Human tra
116	44	55.7	966	8	ADL99369	Adl99369 Nanostruc	189	39	49.4	334	8	ADO22401	Ado22401 Candida a
117	43	54.4	337	5	ABH81634	Abh81634 Human kin	190	39	49.4	435	7	ABO76168	Abv76168 Pseudomon
118	43	54.4	337	5	ABH81634	Abh81634 Human kin	191	39	49.4	451	6	ABU19416	Abu19416 Protein e
119	43	54.4	337	5	ABH81634	Abh81634 Human kin	192	39	49.4	538	8	ADN99667	Adn99667 Novel hum
120	43	54.4	342	5	ABH81634	Abh81634 Human kin	193	39	49.4	792	9	ADBS5349	Adbs5349 Cyclin-de
121	43	54.4	342	6	ADQ23389	Adq23389 Human mot	194	39	49.4	857	9	ADO22399	Ado22399 Cyclin-de
122	43	54.4	342	6	ADQ23389	Adq23389 Human mot	195	39	49.4	857	9	ADO22399	Ado22399 Cyclin-de
123	43	54.4	365	9	ADV50409	Adv50409 Human KIF	196	39	49.4	884	7	ADM56288	Adm56288 Human ATP
124	43	54.4	672	7	ADV69858	Adv69858 Human bea	197	39	49.4	884	9	ADV85875	Adv85875 Zsea may
125	43	54.4	954	8	ADM67697	Adm67697 PRO poly	198	39	49.4	884	9	ADV85875	Adv85875 Zsea may
126	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	199	39	49.4	887	8	ADT60761	Adt60761 Plant pol
127	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	200	39	49.4	928	7	ADT60761	Adt60761 Plant pol
128	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	201	39	49.4	928	7	ADT60761	Adt60761 Plant pol
129	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	202	39	49.4	928	7	ADT60761	Adt60761 Plant pol
130	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	203	39	49.4	928	7	ADT60761	Adt60761 Plant pol
131	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	204	39	49.4	928	7	ADT60761	Adt60761 Plant pol
132	43	54.4	954	8	ADM67697	Adm67697 Rice NACK	205	39	49.4	928	7	ADT60761	Adt60761 Plant pol
133	43	54.4	974	8	ADM67696	Adm67696 A. thalia	206	38.5	48.7	297	4	ABR34053	Abv34053 Human can
134	43	54.4	974	8	ADM67696	Adm67696 A. thalia	207	38	48.1	15	6	ABR34001	Abv34001 Human can
135	43	54.4	1062	8	ADN61178	Adn61178 Radiush nu	208	38	48.1	15	6	ABR34001	Abv34001 Human can
136	43	54.4	1062	8	ADN61178	Adn61178 Radiush nu	209	38	48.1	15	6	ABR33913	Abv33913 Human can
137	43	54.4	1324	7	ADJ95086	Adj95086 Novel NOV	210	38	48.1	15	6	ABR33913	Abv33913 Human can
138	43	54.4	1342	8	ADU73907	Adu73907 Human str	211	38	48.1	15	6	ABR34047	Abv34047 Human can
139	43	54.4	1342	8	ADU73907	Adu73907 Human str	212	38	48.1	15	6	ABR34047	Abv34047 Human can
140	42	53.2	214	8	ADX74336	Adx74336 Plant ful	213	38	48.1	15	6	ABR34046	Abv34046 Human can
141	42	53.2	326	5	ABU99336	Abu99336 Truncated	214	38	48.1	15	6	ABR33945	Abv33945 Human can
142	42	53.2	326	5	ABU99336	Abu99336 Truncated	215	38	48.1	15	6	ABR33945	Abv33945 Human can
143	42	53.2	326	5	ABU99336	Abu99336 Truncated	216	38	48.1	15	6	ABR33945	Abv33945 Human can
144	42	53.2	326	5	ABU99336	Abu99336 Truncated	217	38	48.1	15	6	ABR33945	Abv33945 Human can
145	42	53.2	326	5	ABU99336	Abu99336 Truncated	218	38	48.1	15	6	ABR33945	Abv33945 Human can
146	42	53.2	326	5	ABU99336	Abu99336 Truncated	219	38	48.1	15	6	ABR33945	Abv33945 Human can
147	42	53.2	326	5	ABU99336	Abu99336 Truncated	220	38	48.1	15	6	ABR33945	Abv33945 Human can
148	42	53.2	326	5	ABU99336	Abu99336 Truncated	221	38	48.1	15	6	ABR33945	Abv33945 Human can
149	42	53.2	326	5	ABU99336	Abu99336 Truncated	222	38	48.1	15	6	ABR33945	Abv33945 Human can
150	42	53.2	326	5	ABU99336	Abu99336 Truncated	223	38	48.1	15	6	ABR33945	Abv33945 Human can
151	42	53.2	326	5	ABU99336	Abu99336 Truncated	224	38	48.1	15	6	ABR33945	Abv33945 Human can
152	42	53.2	326	5	ABU99336	Abu99336 Truncated	225	38	48.1	15	6	ABR33945	Abv33945 Human can
153	42	53.2	326	5	ABU99336	Abu99336 Truncated	226	38	48.1	15	6	ABR33945	Abv33945 Human can
154	42	53.2	326	5	ABU99336	Abu99336 Truncated	227	38	48.1	15	6	ABR33945	Abv33945 Human can
155	42	53.2	326	5	ABU99336	Abu99336 Truncated	228	38	48.1	15	6	ABR33945	Abv33945 Human can
156	42	53.2	326	5	ABU99336	Abu99336 Truncated	229	38	48.1	15	6	ABR33945	Abv33945 Human can
157	42	53.2	326	5	ABU99336	Abu99336 Truncated	230	38	48.1	15	6	ABR33945	Abv33945 Human can
158	42	53.2	326	5	ABU99336	Abu99336 Truncated	231	38	48.1	15	6	ABR33945	Abv33945 Human can
159	42	53.2	326	5	ABU99336	Abu99336 Truncated	232	38	48.1	15	6	ABR33945	Abv33945 Human can
160	42	53.2	326	5	ABU99336	Abu99336 Truncated	233	38	48.1	15	6	ABR33945	Abv33945 Human can
161	42	53.2	326	5	ABU99336	Abu99336 Truncated	234	38	48.1	15	6	ABR33945	Abv33945 Human can
162	42	53.2	326	5	ABU99336	Abu99336 Truncated	235	38	48.1	15	6	ABR33945	Abv33945 Human can
163	42	53.2	326	5	ABU99336	Abu99336 Truncated	236	38	48.1	15	6	ABR33945	Abv33945 Human can
164	42	53.2	326	5	ABU99336	Abu99336 Truncated	237	38	48.1	15	6	ABR33945	Abv33945 Human can
165	42	53.2	326	5	ABU99336	Abu99336 Truncated	238	38	48.1	15	6	ABR33945	Abv33945 Human can
166	42	53.2	326	5	ABU99336	Abu99336 Truncated	239	38	48.1	15	6	ABR33945	Abv33945 Human can
167	42	53.2	326	5	ABU99336	Abu99336 Truncated	240	38	48.1	15	6	ABR33945	Abv33945 Human can
168	42	53.2	326	5	ABU99336	Abu99336 Truncated	241	38	48.1	15	6	ABR33945	Abv33945 Human can
169	42	53.2	326	5	ABU99336	Abu99336 Truncated	242	38	48.1	15	6	ABR33945	Abv33945 Human can
170	42	53.2	326	5	ABU99336	Abu99336 Truncated	243	38	48.1	15	6	ABR33945	Abv33945 Human can

244	38	48.1	602	5	ABP43566	Abp43566 Human ehe	317	37	46.8	890	8	ADQ15056	Adq15056 Human can
245	38	48.1	663	4	AAE900221	Aae900221 Human she	318	37	46.8	890	9	ADU46859	Adu46859 RAB6 ince
246	38	48.1	663	4	AAE900221	Aae900221 Human PRO	319	37	46.8	890	9	ADU46859	Adu46859 RAB6 ince
247	38	48.1	663	5	AAU97912	Aau97912 Human mac	320	334	46.8	935	3	AAO13881	Aao13881 Human pol
248	38	48.1	663	7	ADC51455	Adc51455 Human mac	321	37	46.8	957	3	AAO13881	Aao13881 Human pol
249	38	48.1	663	7	ADG25731	Adg25731 Human pro	322	37	46.8	960	3	AAO13881	Aao13881 Human pol
250	38	48.1	680	4	ABG63472	Abg63472 Drosophil	323	37	46.8	960	5	ABG2950	Abg2950 Arabidops
251	38	48.1	718	6	ABU49055	Abu49055 Protein e	324	37	46.8	960	5	ABG30877	Abg30877 A. thalia
252	38	48.1	729	9	ADV77108	Adv77108 Huntingto	325	37	46.8	960	5	ABG30877	Abg30877 A. thalia
253	38	48.1	753	9	ABE40556	Abe40556 L. pneumo	326	37	46.8	993	8	ADQ19013	Adq19013 Human sof
254	38	48.1	774	9	ABE37220	Abe37220 L. pneumo	327	37	46.8	993	8	ADQ19013	Adq19013 Human sof
255	38	48.1	873	8	ADQ76433	Adq76433 Amino aci	328	37	46.8	1016	8	ADR21496	Adr21496 Xenorhabd
256	38	48.1	888	4	AAE06695	Aae06695 Arabidops	329	37	46.8	1016	8	ADR21496	Adr21496 Xenorhabd
257	38	48.1	888	8	ADN72911	Adn72911 Thale cre	330	37	46.8	1029	5	AAE17786	Aae17786 Human kin
258	38	48.1	888	8	ADN73171	Adn73171 Thale cre	331	37	46.8	1029	5	AAE17786	Aae17786 Human kin
259	38	48.1	992	8	ADT57826	Adt57826 Plant pol	332	37	46.8	1034	3	AAO13881	Aao13881 Human pol
260	38	48.1	1030	8	ADY06933	Ady06933 Plant ful	333	37	46.8	1069	3	AAO13881	Aao13881 Human pol
261	38	48.1	1388	5	AAE14400	Aae14400 Human kin	334	37	46.8	1087	6	ABP57673	Abp57673 HIF-1 alp
262	38	48.1	1388	5	AAU79590	Aau79590 Human kin	335	37	46.8	1121	3	AAO13881	Aao13881 Human pol
263	38	48.1	1388	6	ABR48222	AbR48222 Human bla	336	37	46.8	1125	6	ABP57675	Abp57675 HIF-1 alp
264	38	48.1	1388	7	ABR80468	AbR80468 Ovarian c	337	37	46.8	1125	6	ABP57675	Abp57675 HIF-1 alp
265	38	48.1	1388	7	ADC35116	Adc35116 Human bre	338	37	46.8	1160	6	ABP57674	Abp57674 HIF-1 alp
266	38	48.1	1388	8	ADL83290	Adl83290 Human PRO	339	37	46.8	1269	2	AAW03659	Aaw03659 RPP5 down
267	38	48.1	1388	8	ADQ20128	Adq20128 Human sof	340	37	46.8	1274	4	ABE65781	AbE65781 Drosophil
268	38	48.1	1388	8	ADQ09226	AdQ09226 Human RNS	341	37	46.8	1274	9	ABE65781	AbE65781 Drosophil
269	38	48.1	1388	9	AEA62054	Aea62054 Human kin	342	37	46.8	1474	7	AAE39593	Aae39593 Drosophil
270	37	46.8	64	4	AAU43043	Aau43043 Propionib	343	37	46.8	1500	4	ABE63715	AbE63715 Drosophil
271	37	46.8	64	6	ABM39562	Abm39562 Propionib	344	37	46.8	1503	7	AAE39594	Aae39594 Drosophil
272	37	46.8	87	4	ABG65040	Abg65040 Drosophil	345	37	46.8	1509	7	AAE39592	Aae39592 Drosophil
273	37	46.8	87	8	ADQ07971	AdQ07971 Fly poly	346	36.5	46.2	3138	4	ABE61958	AbE61958 Drosophil
274	37	46.8	120	8	ADQ07971	AdQ07971 Phosphona	347	36	45.6	247	4	ABG23162	Abg23162 Novel hum
275	37	46.8	137	2	AAW64594	Aaw64594 Rabbit J	348	36	45.6	61	3	AAQ00127	Aaq00127 Human sec
276	37	46.8	137	2	AAW61573	Aaw61573 Rabbit J	349	36	45.6	72	4	ABE41362	AbE41362 Peptide #
277	37	46.8	137	2	AAW85747	Aaw85747 J chain s	350	36	45.6	72	4	AAW35150	Aaw35150 Peptide #
278	37	46.8	137	5	ABG94816	Abg94816 Rabbit J	351	36	45.6	72	4	ABE25299	AbE25299 Protein #
279	37	46.8	137	5	ABG68245	Abg68245 Rabbit J	352	36	45.6	72	4	AAW75034	Aaw75034 Human bon
280	37	46.8	137	8	ADH61859	Adh61859 Mouse J c	353	36	45.6	72	4	AAU59486	Aau59486 Propionib
281	37	46.8	159	2	AAW71890	Aaw71890 Anti-huma	354	36	45.6	72	4	ABG56803	Abg56803 Human liv
282	37	46.8	159	3	AAE12910	Aae12910 Anti-huma	355	36	45.6	72	6	ABM56005	Abm56005 Propionib
283	37	46.8	209	4	ABG03132	Abg03132 Novel hum	356	36	45.6	79	5	ABP38302	Abp38302 Staphyloc
284	37	46.8	290	7	ADM25686	Adm25686 Hyperther	357	36	45.6	79	8	ADQ4766	Adq4766 Staphyloc
285	37	46.8	329	5	AAE17787	Aae17787 Human kin	358	36	45.6	88	4	AAU48647	Aau48647 Propionib
286	37	46.8	382	8	ADQ05898	AdQ05898 C. albica	359	36	45.6	88	6	ABM45166	Abm45166 Propionib
287	37	46.8	382	8	ADQ05894	AdQ05894 C. albica	360	36	45.6	99	4	AAU54137	Aau54137 Propionib
288	37	46.8	431	8	ADN21136	Adn21136 Bacterial	361	36	45.6	99	6	ABM50656	Abm50656 Propionib
289	37	46.8	431	6	ABH85506	Abh85506 Human pro	362	36	45.6	182	8	ADS44591	Ads44591 Bacterial
290	37	46.8	445	6	ABU21623	Abu21623 Protein e	363	36	45.6	188	7	ABO67490	AbO67490 Klebsiell
291	37	46.8	457	9	ABM92762	Abm92762 M. xanthu	364	36	45.6	204	5	ABH48449	Abh48449 Listeria
292	37	46.8	490	4	ABG23354	Abg23354 Novel hum	365	36	45.6	248	2	AAW72906	Aaw72906 Mycobacte
293	37	46.8	500	3	AAE21939	Aae21939 Arabidops	366	36	45.6	248	2	AAE21923	Aae21923 Amino aci
294	37	46.8	528	6	ABU56420	Abu56420 Lung canc	367	36	45.6	299	6	ABU22539	Abu22539 Protein e
295	37	46.8	528	7	ADH80539	Adh80539 Ovarian c	368	36	45.6	317	6	ABP57736	Abp57736 S. pombe
296	37	46.8	538	8	ADQ05892	AdQ05892 C. albica	369	36	45.6	321	4	ABE52869	AbE52869 Escherich
297	37	46.8	538	8	ADQ05896	AdQ05896 C. albica	370	36	45.6	340	9	ADW46619	Adw46619 Salmonid
298	37	46.8	545	8	ABO59509	AbO59509 Human gen	371	36	45.6	361	5	ABH08099	Abh08099 Human HSE
299	37	46.8	575	3	AAE21938	Aae21938 Arabidops	372	36	45.6	361	5	ABH08099	Abh08099 Human HSE
300	37	46.8	578	3	ABO64082	AbO64082 Klebsiell	373	36	45.6	361	8	ADS13628	Ads13628 Human HSE
301	37	46.8	598	3	AAE21937	Aae21937 Arabidops	374	36	45.6	369	5	ABH08101	Abh08101 Human HSE
302	37	46.8	600	9	ADY49879	Ady49879 Fumarate	375	36	45.6	369	6	ABU63120	Abu63120 Human kin
303	37	46.8	602	9	ADY45237	Ady45237 Bacterial	376	36	45.6	369	8	ADS13632	Ads13632 Human HSE
304	37	46.8	602	9	ADY80487	Ady80487 Non-amino	377	36	45.6	370	5	ABH08100	Abh08100 Human HSE
305	37	46.8	627	2	AAW85710	Aaw85710 Grand fir	378	36	45.6	370	5	ABU63119	Abu63119 Human kin
306	37	46.8	627	4	AAW69380	Aaw69380 Grand fir	379	36	45.6	370	8	ADS13630	Ads13630 Human HSE
307	37	46.8	627	5	ABH79395	Abh79395 Taxadiene	380	36	45.6	374	8	ADQ67675	Adq67675 Novel hum
308	37	46.8	729	4	ABH59500	Abh59500 Drosophil	381	36	45.6	375	9	AAE17501	Aae17501 Brassica
309	37	46.8	811	6	ABR58290	AbR58290 BCU0343 p	382	36	45.6	384	2	AAE34649	Aae34649 Heparinas
310	37	46.8	811	6	ABR58329	AbR58329 XM_035861	383	36	45.6	384	2	AAW28545	Aaw28545 Mutant po
311	37	46.8	865	6	ABR41371	AbR41371 Human DIT	384	36	45.6	384	3	AAW70186	Aaw70186 Mutant F.
312	37	46.8	868	6	ABR41418	AbR41418 Human DIT	385	36	45.6	384	3	AAW70195	Aaw70195 Mutant F.
313	37	46.8	870	5	ABP69487	Abp69487 Human pol	386	36	45.6	384	3	AAW70174	Aaw70174 Modified
314	37	46.8	884	6	ABU05307	Abu05307 Human dia	387	36	45.6	384	3	AAW70190	Aaw70190 Mutant F.
315	37	46.8	890	6	ABR922143	AbR922143 Human cer	388	36	45.6	384	3	AAW70180	Aaw70180 Mutant F.
316	37	46.8	890	8	ADQ09274	AdQ09274 Human RAB	389	36	45.6	384	3	AAW70184	Aaw70184 Mutant F.

390	36	45.6	384	3	AAy70187	AAy70187 Mutant F.	463	36	45.6	1815	8	ADR66952	Human pro
391	36	45.6	384	3	AAy70159	AAy70159 F. hepari	464	36	45.6	1815	8	ADR66054	Human pro
392	36	45.6	384	3	AAy70189	AAy70189 Mutant F.	465	36	45.6	1815	8	ADR66951	Human pro
393	36	45.6	384	3	AAy70192	AAy70192 Mutant F.	466	36	45.6	1815	8	ADR66053	Human pro
394	36	45.6	384	3	AAy70175	AAy70175 Mutant F.	467	36	45.6	1826	7	ADU69671	Human hea
395	36	45.6	384	3	AAy70193	AAy70193 Mutant F.	468	36	45.6	1826	7	ADL83235	Human PRO
396	36	45.6	384	3	AAy70176	AAy70176 Mutant F.	469	36	45.6	1844	8	ADQ97522	Mouse can
397	36	45.6	384	3	AAy70183	AAy70183 Mutant F.	470	36	45.6	2732	7	ABM86028	Rice abio
398	36	45.6	384	3	AAy70188	AAy70188 Mutant F.	471	35	5	456	4	ABB66306	Drosophil
399	36	45.6	384	3	AAy70178	AAy70178 Mutant F.	472	35	44.9	456	2	AAE51685	Basophil
400	36	45.6	384	3	AAy70177	AAy70177 Mutant F.	473	35	44.3	11	2	ABG20543	Novel hum
401	36	45.6	384	3	AAy70194	AAy70194 Mutant F.	474	35	44.3	117	4	ABG20543	Novel hum
402	36	45.6	384	3	AAy70179	AAy70179 Mutant F.	475	35	44.3	122	4	ABG20543	Novel hum
403	36	45.6	384	3	AAy70182	AAy70182 Mutant F.	476	35	44.3	122	4	ABG20543	Novel hum
404	36	45.6	384	3	AAy70181	AAy70181 Mutant F.	477	35	44.3	126	6	ABM72416	Staphyloc
405	36	45.6	384	3	AAy70191	AAy70191 Mutant F.	478	35	44.3	130	4	AAU30136	Novel hum
406	36	45.6	384	3	AAy70185	AAy70185 Mutant F.	479	35	44.3	137	3	ABG25350	Pinus rad
407	36	45.6	384	4	ABM6931	ABM6931 Flavobact	480	35	44.3	138	4	AAU46015	Propionib
408	36	45.6	384	4	ABM6931	ABM6931 Pedobacte	481	35	44.3	138	6	ABM42534	Human EST
409	36	45.6	401	5	ABU05531	ABU05531 M. tuberc	482	35	44.3	158	4	ABM42534	Human EST
410	36	45.6	415	4	ABU05531	ABU05531 M. tuberc	483	35	44.3	162	4	ABM42534	Human EST
411	36	45.6	421	4	ABM70452	ABM70452 Drosophil	484	35	44.3	165	5	ABM42534	Human EST
412	36	45.6	423	7	ABM70452	ABM70452 Drosophil	485	35	44.3	165	5	ABM42534	Human EST
413	36	45.6	433	8	ABM70452	ABM70452 Drosophil	486	35	44.3	165	5	ABM42534	Human EST
414	36	45.6	445	8	ABM70452	ABM70452 Drosophil	487	35	44.3	165	5	ABM42534	Human EST
415	36	45.6	475	8	ABM70452	ABM70452 Drosophil	488	35	44.3	165	5	ABM42534	Human EST
416	36	45.6	503	3	ABM70452	ABM70452 Drosophil	489	35	44.3	165	5	ABM42534	Human EST
417	36	45.6	519	9	ABM70452	ABM70452 Drosophil	490	35	44.3	165	5	ABM42534	Human EST
418	36	45.6	531	9	ABM70452	ABM70452 Drosophil	491	35	44.3	165	5	ABM42534	Human EST
419	36	45.6	581	9	ABM70452	ABM70452 Drosophil	492	35	44.3	165	5	ABM42534	Human EST
420	36	45.6	626	4	ABM70452	ABM70452 Drosophil	493	35	44.3	165	5	ABM42534	Human EST
421	36	45.6	626	4	ABM70452	ABM70452 Drosophil	494	35	44.3	165	5	ABM42534	Human EST
422	36	45.6	666	8	ABM70452	ABM70452 Drosophil	495	35	44.3	165	5	ABM42534	Human EST
423	36	45.6	666	8	ABM70452	ABM70452 Drosophil	496	35	44.3	165	5	ABM42534	Human EST
424	36	45.6	666	8	ABM70452	ABM70452 Drosophil	497	35	44.3	165	5	ABM42534	Human EST
425	36	45.6	673	8	ABM70452	ABM70452 Drosophil	498	35	44.3	165	5	ABM42534	Human EST
426	36	45.6	673	8	ABM70452	ABM70452 Drosophil	499	35	44.3	165	5	ABM42534	Human EST
427	36	45.6	674	4	ABM70452	ABM70452 Drosophil	500	35	44.3	165	5	ABM42534	Human EST
428	36	45.6	684	4	ABM70452	ABM70452 Drosophil	501	35	44.3	165	5	ABM42534	Human EST
429	36	45.6	696	7	ABM70452	ABM70452 Drosophil	502	35	44.3	165	5	ABM42534	Human EST
430	36	45.6	743	8	ABM70452	ABM70452 Drosophil	503	35	44.3	165	5	ABM42534	Human EST
431	36	45.6	753	4	ABM70452	ABM70452 Drosophil	504	35	44.3	165	5	ABM42534	Human EST
432	36	45.6	753	4	ABM70452	ABM70452 Drosophil	505	35	44.3	165	5	ABM42534	Human EST
433	36	45.6	757	5	ABM70452	ABM70452 Drosophil	506	35	44.3	165	5	ABM42534	Human EST
434	36	45.6	757	5	ABM70452	ABM70452 Drosophil	507	35	44.3	165	5	ABM42534	Human EST
435	36	45.6	762	5	ABM70452	ABM70452 Drosophil	508	35	44.3	165	5	ABM42534	Human EST
436	36	45.6	776	4	ABM70452	ABM70452 Drosophil	509	35	44.3	165	5	ABM42534	Human EST
437	36	45.6	782	4	ABM70452	ABM70452 Drosophil	510	35	44.3	165	5	ABM42534	Human EST
438	36	45.6	803	7	ABM70452	ABM70452 Drosophil	511	35	44.3	165	5	ABM42534	Human EST
439	36	45.6	803	7	ABM70452	ABM70452 Drosophil	512	35	44.3	165	5	ABM42534	Human EST
440	36	45.6	859	8	ABM70452	ABM70452 Drosophil	513	35	44.3	165	5	ABM42534	Human EST
441	36	45.6	904	6	ABM70452	ABM70452 Drosophil	514	35	44.3	165	5	ABM42534	Human EST
442	36	45.6	915	6	ABM70452	ABM70452 Drosophil	515	35	44.3	165	5	ABM42534	Human EST
443	36	45.6	984	6	ABM70452	ABM70452 Drosophil	516	35	44.3	165	5	ABM42534	Human EST
444	36	45.6	1038	5	ABM70452	ABM70452 Drosophil	517	35	44.3	165	5	ABM42534	Human EST
445	36	45.6	1264	5	ABM70452	ABM70452 Drosophil	518	35	44.3	165	5	ABM42534	Human EST
446	36	45.6	1307	5	ABM70452	ABM70452 Drosophil	519	35	44.3	165	5	ABM42534	Human EST
447	36	45.6	1313	8	ABM70452	ABM70452 Drosophil	520	35	44.3	165	5	ABM42534	Human EST
448	36	45.6	1362	5	ABM70452	ABM70452 Drosophil	521	35	44.3	165	5	ABM42534	Human EST
449	36	45.6	1427	9	ABM70452	ABM70452 Drosophil	522	35	44.3	165	5	ABM42534	Human EST
450	36	45.6	1460	3	ABM70452	ABM70452 Drosophil	523	35	44.3	165	5	ABM42534	Human EST
451	36	45.6	1462	3	ABM70452	ABM70452 Drosophil	524	35	44.3	165	5	ABM42534	Human EST
452	36	45.6	1507	8	ABM70452	ABM70452 Drosophil	525	35	44.3	165	5	ABM42534	Human EST
453	36	45.6	1518	3	ABM70452	ABM70452 Drosophil	526	35	44.3	165	5	ABM42534	Human EST
454	36	45.6	1604	3	ABM70452	ABM70452 Drosophil	527	35	44.3	165	5	ABM42534	Human EST
455	36	45.6	1606	3	ABM70452	ABM70452 Drosophil	528	35	44.3	165	5	ABM42534	Human EST
456	36	45.6	1649	7	ABM70452	ABM70452 Drosophil	529	35	44.3	165	5	ABM42534	Human EST
457	36	45.6	1662	3	ABM70452	ABM70452 Drosophil	530	35	44.3	165	5	ABM42534	Human EST
458	36	45.6	1769	8	ABM70452	ABM70452 Drosophil	531	35	44.3	165	5	ABM42534	Human EST
459	36	45.6	1780	4	ABM70452	ABM70452 Drosophil	532	35	44.3	165	5	ABM42534	Human EST
460	36	45.6	1780	4	ABM70452	ABM70452 Drosophil	533	35	44.3	165	5	ABM42534	Human EST
461	36	45.6	1788	4	ABM70452	ABM70452 Drosophil	534	35	44.3	165	5	ABM42534	Human EST
462	36	45.6	1805	5	ABM70452	ABM70452 Drosophil	535	35	44.3	165	5	ABM42534	Human EST

536	35	44.3	340	9	ADW46644	Adw46644	Salmonid	609	35	44.3	348	3	AAG27818	Aeg27818	Arabidops
537	35	44.3	340	9	ADW46650	Adw46650	Salmonid	610	35	44.3	350	8	ADN04058	Adn04058	Antipsori
538	35	44.3	340	9	ADW46652	Adw46652	Salmonid	611	35	44.3	350	9	ADX06150	Adx06150	Cyclin-de
539	35	44.3	340	9	ADW46606	Adw46606	Salmonid	612	35	44.3	362	6	ABU00077	Abu00077	Human nov
540	35	44.3	340	9	ADW46612	Adw46612	Salmonid	613	35	44.3	365	9	ADV50414	Adv50414	Human KIF
541	35	44.3	340	9	ADW46625	Adw46625	Salmonid	614	35	44.3	369	7	ADU08029	Adu08029	Novel pro
542	35	44.3	340	9	ADW46627	Adw46627	Salmonid	615	35	44.3	369	9	ADU40399	Adu40399	Novel hum
543	35	44.3	340	9	ADW46639	Adw46639	Salmonid	616	35	44.3	370	4	ABG23842	Abg23842	Novel hum
544	35	44.3	340	9	ADW46589	Adw46589	Salmonid	617	35	44.3	372	7	ABE61903	AbE61903	Rat Prote
545	35	44.3	340	9	ADW46591	Adw46591	Salmonid	618	35	44.3	381	6	ABU00078	Abu00078	Human nov
546	35	44.3	340	9	ADW46614	Adw46614	Salmonid	619	35	44.3	394	5	AAO17206	Aao17206	Human sec
547	35	44.3	340	9	ADW46643	Adw46643	Salmonid	620	35	44.3	394	5	ABG64749	Abg64749	Human alb
548	35	44.3	340	9	ADW46658	Adw46658	Salmonid	621	35	44.3	394	8	ADL78016	Adl78016	Albumin f
549	35	44.3	340	9	ADW46662	Adw46662	Salmonid	622	35	44.3	395	7	ADM05932	Adm05932	Human pro
550	35	44.3	340	9	ADW46594	Adw46594	Salmonid	623	35	44.3	399	3	AAG27817	Aag27817	Arabidops
551	35	44.3	340	9	ADW46598	Adw46598	Salmonid	624	35	44.3	404	6	ADA35193	Ada35193	Acinetoba
552	35	44.3	340	9	ADW46629	Adw46629	Salmonid	625	35	44.3	407	9	ADU40584	Adu40584	Novel hum
553	35	44.3	340	9	ADW46636	Adw46636	Salmonid	626	35	44.3	408	7	ADC21265	Adc21265	Plasmodi
554	35	44.3	340	9	ADW46588	Adw46588	Salmonid	627	35	44.3	412	5	ABP53641	Abp53641	Medicago
555	35	44.3	340	9	ADW46605	Adw46605	Salmonid	628	35	44.3	414	8	ADX71432	Adx71432	Plant ful
556	35	44.3	340	9	ADW46609	Adw46609	Salmonid	629	35	44.3	419	4	AAW44997	Aaw44997	Human sec
557	35	44.3	340	9	ADW46646	Adw46646	Salmonid	630	35	44.3	421	4	AAW41820	Aaw41820	Human pol
558	35	44.3	340	9	ADW46603	Adw46603	Salmonid	631	35	44.3	422	8	ADT57719	Adt57719	Plant pol
559	35	44.3	340	9	ADW46653	Adw46653	Salmonid	632	35	44.3	435	7	ABO63465	AbO63465	Klebsiell
560	35	44.3	340	9	ADW46585	Adw46585	Salmonid	633	35	44.3	439	7	ADM05041	Adm05041	Human pro
561	35	44.3	340	9	ADW46607	Adw46607	Salmonid	634	35	44.3	443	4	AAU30139	Aau30139	Novel hum
562	35	44.3	340	9	ADW46615	Adw46615	Salmonid	635	35	44.3	444	8	ADX92254	Adx92254	Plant ful
563	35	44.3	340	9	ADW46617	Adw46617	Salmonid	636	35	44.3	450	4	AAW464208	Aaw464208	Murine pr
564	35	44.3	340	9	ADW46623	Adw46623	Salmonid	637	35	44.3	450	8	ADX92628	Adx92628	Plant ful
565	35	44.3	340	9	ADW46631	Adw46631	Salmonid	638	35	44.3	454	4	AAU54429	Aau54429	Propionib
566	35	44.3	340	9	ADW46654	Adw46654	Salmonid	639	35	44.3	454	6	ABM50948	Abm50948	Propionib
567	35	44.3	340	9	ADW46559	Adw46559	Salmonid	640	35	44.3	468	5	ABG97352	Abg97352	Human CGD
568	35	44.3	340	9	ADW46663	Adw46663	Salmonid	641	35	44.3	473	5	ABG70992	Abg70992	Human car
569	35	44.3	340	9	ADW46586	Adw46586	Salmonid	642	35	44.3	474	7	ABM86533	Abm86533	Rice abio
570	35	44.3	340	9	ADW46596	Adw46596	Salmonid	643	35	44.3	479	9	ABE38253	AbE38253	L. pneumo
571	35	44.3	340	9	ADW46602	Adw46602	Salmonid	644	35	44.3	481	8	ADX73714	Adx73714	Plant ful
572	35	44.3	340	9	ADW46635	Adw46635	Salmonid	645	35	44.3	495	4	AAW44224	Aaw44224	Human pro
573	35	44.3	340	9	ADW46637	Adw46637	Salmonid	646	35	44.3	506	5	AAE21173	Aae21173	Human TRI
574	35	44.3	340	9	ADW46641	Adw46641	Salmonid	647	35	44.3	522	5	ABG70991	Abg70991	Human HAK
575	35	44.3	340	9	ADW46647	Adw46647	Salmonid	648	35	44.3	549	8	ADY12421	Ady12421	Plant ful
576	35	44.3	340	9	ADW46655	Adw46655	Salmonid	649	35	44.3	549	8	ADY08818	Ady08818	Plant ful
577	35	44.3	340	9	ADW46590	Adw46590	Salmonid	650	35	44.3	550	4	ABG16717	Abg16717	Novel hum
578	35	44.3	340	9	ADW46593	Adw46593	Salmonid	651	35	44.3	554	7	ADJ71145	Adj71145	Human hea
579	35	44.3	340	9	ADW46608	Adw46608	Salmonid	652	35	44.3	562	8	ADS21149	AdS21149	Bacterial
580	35	44.3	340	9	ADW46642	Adw46642	Salmonid	653	35	44.3	563	8	ADN18322	Adn18322	Bacterial
581	35	44.3	340	9	ADW46645	Adw46645	Salmonid	654	35	44.3	571	8	ADN17386	Adn17386	Bacterial
582	35	44.3	340	9	ADW46664	Adw46664	Salmonid	655	35	44.3	628	4	ABE62327	AbE62327	Drosophil
583	35	44.3	340	9	ADW46561	Adw46561	Salmonid	656	35	44.3	631	6	ADB07316	AdB07316	Alloloco
584	35	44.3	340	9	ADW46597	Adw46597	Salmonid	657	35	44.3	632	3	AAV66689	Aav66689	Membrane-
585	35	44.3	340	9	ADW46604	Adw46604	Salmonid	658	35	44.3	632	3	AAAB01385	AaAB01385	Neuron-as
586	35	44.3	340	9	ADW46632	Adw46632	Salmonid	659	35	44.3	632	4	AAW78630	Aaw78630	Plasmolem
587	35	44.3	340	9	ADW46634	Adw46634	Salmonid	660	35	44.3	632	4	AAU29106	Aau29106	Human PRO
588	35	44.3	340	9	ADW46601	Adw46601	Salmonid	661	35	44.3	632	4	AAW39084	Aaw39084	Human pol
589	35	44.3	340	9	ADW46628	Adw46628	Salmonid	662	35	44.3	632	4	AAW87545	Aaw87545	Human PRO
590	35	44.3	340	9	ADW46665	Adw46665	Salmonid	663	35	44.3	632	4	AAW65212	Aaw65212	Human PRO
591	35	44.3	340	9	ADW46595	Adw46595	Salmonid	664	35	44.3	632	5	ABG95870	Abg95870	Human sec
592	35	44.3	340	9	ADW46600	Adw46600	Salmonid	665	35	44.3	632	6	ABU58482	Abu58482	Human PRO
593	35	44.3	340	9	ADW46610	Adw46610	Salmonid	666	35	44.3	632	6	ABU88030	Abu88030	Novel hum
594	35	44.3	340	9	ADW46611	Adw46611	Salmonid	667	35	44.3	632	6	ABU84345	Abu84345	Human sec
595	35	44.3	340	9	ADW46616	Adw46616	Salmonid	668	35	44.3	632	6	ABR66219	AbR66219	Human sec
596	35	44.3	340	9	ADW46621	Adw46621	Salmonid	669	35	44.3	632	6	ABR65609	AbR65609	Human sec
597	35	44.3	340	9	ADW46640	Adw46640	Salmonid	670	35	44.3	632	6	ABU99549	Abu99549	Human sec
598	35	44.3	340	9	ADW46660	Adw46660	Salmonid	671	35	44.3	632	6	ABU58027	Abu58027	Human PRO
599	35	44.3	340	9	ADW46667	Adw46667	Salmonid	672	35	44.3	632	6	ABU59105	Abu59105	Novel hum
600	35	44.3	340	9	ADW46587	Adw46587	Salmonid	673	35	44.3	632	6	ABU82617	Abu82617	Human sec
601	35	44.3	340	9	ADW46630	Adw46630	Salmonid	674	35	44.3	632	6	ABU82788	Abu82788	Human PRO
602	35	44.3	340	9	ADW46638	Adw46638	Salmonid	675	35	44.3	632	6	ABU89909	Abu89909	Novel hum
603	35	44.3	340	9	ADW46657	Adw46657	Salmonid	676	35	44.3	632	6	ABR68158	AbR68158	Human sec
604	35	44.3	340	9	ADW46613	Adw46613	Salmonid	677	35	44.3	632	6	ABU60536	Abu60536	Human sec
605	35	44.3	340	9	ADW46622	Adw46622	Salmonid	678	35	44.3	632	6	ABU96211	Abu96211	Novel hum
606	35	44.3	340	9	ADW46651	Adw46651	Salmonid	679	35	44.3	632	6	ABU92642	Abu92642	Human sec
607	35	44.3	340	9	ADW22678	Adw22678	Sleeping	680	35	44.3	632	6	ABO08719	AbO08719	Human sec
608	35	44.3	340	9	ADW03280	Adw03280	Sleeping	681	35	44.3	632	6	ABO02771	AbO02771	Human sec

682	35	44.3	632	6	ABR74925	Human sec	AbR74925	Human sec	755	35	44.3	632	6	ABU82252	Novel hum
683	35	44.3	632	6	ABR94687	Human sec	AbR94687	Human sec	756	35	44.3	632	6	ABU87263	Human PRO
684	35	44.3	632	6	ABU13918	Human PRO	AbU13918	Human PRO	757	35	44.3	632	6	ABU83735	Human sec
685	35	44.3	632	6	ABU85660	Human PRO	Abu85660	Human PRO	758	35	44.3	632	6	ABO08109	Human PRO
686	35	44.3	632	6	ABU98820	Novel hum	Abu98820	Novel hum	759	35	44.3	632	6	ABU92495	Human sec
687	35	44.3	632	6	ABU988035	Novel hum	Abu98035	Novel hum	760	35	44.3	632	6	ABU81820	Novel hum
688	35	44.3	632	6	ABU91741	Novel hum	Abu91741	Novel hum	761	35	44.3	632	6	ABU65984	Human sec
689	35	44.3	632	6	ABU89434	Human PRO	Abu89434	Human PRO	762	35	44.3	632	6	ABU81165	Human sec
690	35	44.3	632	6	ABU86275	Human sec	Abu86275	Human sec	763	35	44.3	632	6	ABU94001	Novel hum
691	35	44.3	632	6	ABU67488	Human PRO	Abu67488	Human PRO	764	35	44.3	632	6	ABU99854	Human sec
692	35	44.3	632	6	ABU080516	Novel hum	Abu72503	Novel hum	765	35	44.3	632	6	ABR66524	Human sec
693	35	44.3	632	6	ABU072503	Novel hum	Abu90895	Novel hum	766	35	44.3	632	6	ABR90942	Human sec
694	35	44.3	632	6	ABU90895	Novel hum	Abu33954	Human sec	767	35	44.3	632	6	ABO53280	Novel hum
695	35	44.3	632	6	ABO33954	Human sec	AbR98824	Human sec	768	35	44.3	632	6	ABU58958	Human sec
696	35	44.3	632	6	ABR99434	Human sec	Abu16347	Human sec	769	35	44.3	632	6	ABU94369	Human PRO
697	35	44.3	632	6	ABR98824	Human sec	Abu8888	Human sec	770	35	44.3	632	6	ABU79251	Human PRO
698	35	44.3	632	6	ABO16347	Human sec	AbR92247	Human sec	771	35	44.3	632	6	ABU86580	Novel hum
699	35	44.3	632	6	ABR92247	Human sec	Abu18888	Human sec	772	35	44.3	632	6	ABU86885	Novel hum
700	35	44.3	632	6	ABO18888	Human sec	AbR78309	Human sec	773	35	44.3	632	6	ABU94674	Human PRO
701	35	44.3	632	6	ABR78309	Human sec	AbU71971	Novel hum	774	35	44.3	632	6	ABU84601	Human PRO
702	35	44.3	632	6	ABU71971	Novel hum	Abu85045	Novel hum	775	35	44.3	632	6	ABR70350	Human sec
703	35	44.3	632	6	ABU85045	Novel hum	Abu00184	Novel hum	776	35	44.3	632	6	ABU92336	Novel hum
704	35	44.3	632	6	ABO00184	Novel hum	Abu11516	Human sec	777	35	44.3	632	6	ABU98515	Human PRO
705	35	44.3	632	6	ABO11516	Human sec	Abu02161	Human sec	778	35	44.3	632	6	ABU98515	Human PRO
706	35	44.3	632	6	ABO02161	Human sec	Abu88735	Novel hum	779	35	44.3	632	6	ABR65914	Human sec
707	35	44.3	632	6	ABU88735	Novel hum	Abu3430	Human sec	780	35	44.3	632	6	ABR64631	Human sec
708	35	44.3	632	6	ABU83430	Human sec	Abu6231	Novel hum	781	35	44.3	632	6	ABU59401	Novel hum
709	35	44.3	632	6	ABO06231	Novel hum	AbR59267	Human sec	782	35	44.3	632	6	ABU79556	Human sec
710	35	44.3	632	6	ABR59267	Human sec	Abu09329	Human sec	783	35	44.3	632	6	ABU92947	Human sec
711	35	44.3	632	6	ABO09329	Human sec	Abu19193	Novel hum	784	35	44.3	632	6	ABU95906	Human PRO
712	35	44.3	632	6	ABO19193	Novel hum	Abu11211	Human sec	785	35	44.3	632	6	ABU91126	Novel hum
713	35	44.3	632	6	ABO11211	Human sec	AbR68829	Human sec	786	35	44.3	632	6	ABU90219	Novel hum
714	35	44.3	632	6	ABR68829	Human sec	Abu16042	Human sec	787	35	44.3	632	6	ABO09634	Human sec
715	35	44.3	632	6	ABO16042	Human sec	Abu13748	Human sec	788	35	44.3	632	6	ABO10906	Human sec
716	35	44.3	632	6	ABU13748	Human sec	Abu71525	Human sec	789	35	44.3	632	6	ABR70960	Human sec
717	35	44.3	632	6	ABU71525	Human sec	Abu65651	Human sec	790	35	44.3	632	6	ABU98282	Novel hum
718	35	44.3	632	6	ABU65651	Human sec	Abu07499	Human PRO	791	35	44.3	632	6	ABu91436	Human PRO
719	35	44.3	632	6	ABO07499	Human PRO	Abu03686	Human sec	792	35	44.3	632	6	ABU89287	Novel hum
720	35	44.3	632	6	ABO03686	Human sec	Abu67134	Human sec	793	35	44.3	632	6	ABU84650	Human sec
721	35	44.3	632	6	ABR67134	Human sec	Abu15737	Human sec	794	35	44.3	632	6	ABR69740	Human PRO
722	35	44.3	632	6	ABO15737	Human sec	Abu56018	Human sec	795	35	44.3	632	6	ABU80117	Human PRO
723	35	44.3	632	6	ABU56018	Human sec	Abu72306	Human PRO	796	35	44.3	632	6	ABU82494	Novel hum
724	35	44.3	632	6	ABU72306	Human PRO	Abu65346	Human PRO	797	35	44.3	632	6	ABU92167	Novel hum
725	35	44.3	632	6	ABU65346	Human PRO	Abu95291	Novel hum	798	35	44.3	632	6	ABU93386	Human PRO
726	35	44.3	632	6	ABU95291	Novel hum	Abu71194	Human PRO	799	35	44.3	632	6	ABO09939	Human sec
727	35	44.3	632	6	ABU71194	Human PRO	Abu07804	Human PRO	800	35	44.3	632	6	ABO09024	Human sec
728	35	44.3	632	6	ABO07804	Human PRO	Abu70045	Human sec	801	35	44.3	632	6	ABU96458	Human PRO
729	35	44.3	632	6	ABR70045	Human sec	AbR69378	Human sec	802	35	44.3	632	6	ABU96458	Human PRO
730	35	44.3	632	6	ABR69378	Human sec	Abu01519	Human PRO	803	35	44.3	632	6	ABU10873	Human PRO
731	35	44.3	632	6	ABO01519	Human PRO	Abu81321	Human PRO	804	35	44.3	632	6	ABU10592	Human sec
732	35	44.3	632	6	ABU81321	Human PRO	AbR60118	Human sec	805	35	44.3	632	6	ABU81625	Novel hum
733	35	44.3	632	6	ABR60118	Human sec	Abu90529	Novel hum	806	35	44.3	632	6	ABU72128	Human PRO
734	35	44.3	632	6	ABU90529	Novel hum	Abu89045	Human sec	807	35	44.3	632	6	ABU95601	Human PRO
735	35	44.3	632	6	ABU89045	Human sec	AbR7853	Human sec	808	35	44.3	632	6	ABU96810	Novel hum
736	35	44.3	632	6	ABR7853	Human sec	AbR65241	Human sec	809	35	44.3	632	6	ABR70655	Human sec
737	35	44.3	632	6	ABR65241	Human sec	AbR68463	Human sec	810	35	44.3	632	6	ABO05006	Novel hum
738	35	44.3	632	6	ABR68463	Human sec	Abu71875	Human sec	811	35	44.3	632	6	ABO08414	Human sec
739	35	44.3	632	6	ABR71875	Human sec	Abu59252	Human sec	812	35	44.3	632	6	ABU88564	Human PRO
740	35	44.3	632	6	ABU59252	Human sec	Abu85355	Human PRO	813	35	44.3	632	6	ABO34078	Human PRO
741	35	44.3	632	6	ABU85355	Human PRO	Abu83125	Human sec	814	35	44.3	632	6	ABO05621	Human sec
742	35	44.3	632	6	ABU83125	Human sec	Abu94981	Novel hum	815	35	44.3	632	6	ABR74010	Human sec
743	35	44.3	632	6	ABU94981	Novel hum	Abu90529	Novel hum	816	35	44.3	632	6	ABR75602	Human sec
744	35	44.3	632	6	ABU90529	Novel hum	Abu93691	Novel hum	817	35	44.3	632	6	ABR80899	Human sec
745	35	44.3	632	6	ABU84040	Human sec	Abu84040	Human sec	818	35	44.3	632	6	ABR81204	Human sec
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753	35	44.3	632	6	ABU57013	Human PRO	Abu55965	Novel hum	826	35	44.3	632	6	ABO35874	Human PRO
754	35	44.3	632	6	ABU55965	Novel hum			827	35	44.3	632	6	ABO44013	Human PRO

828	35	44.3	632	6	ADA77918	Human	sec	Ada77918	Human	sec	901	35	44.3	632	6	ABM04255	Human	sec	Abm04255	Human	sec
829	35	44.3	632	6	ABM24808	Human	sec	Abm24808	Human	sec	902	35	44.3	632	6	ABM22368	Human	sec	Abm22368	Human	sec
830	35	44.3	632	6	ABO03076	Human	sec	AbO03076	Human	sec	903	35	44.3	632	6	ABM07664	Human	sec	Abm07664	Human	sec
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835	35	44.3	632	6	ADB17097	Human	tra	AdB17097	Human	tra	908	35	44.3	632	6	ABO50250	Human	sec	AbO50250	Human	sec
836	35	44.3	632	6	ABO21535	Human	sec	AbO21535	Human	sec	909	35	44.3	632	6	ABU99244	Human	sec	AbU99244	Human	sec
837	35	44.3	632	6	ABR97799	Human	sec	AbR97799	Human	sec	910	35	44.3	632	6	ABO04296	Human	sec	AbO04296	Human	sec
838	35	44.3	632	6	ABR87587	Human	sec	AbR87587	Human	sec	911	35	44.3	632	6	ABO05926	Human	sec	AbO05926	Human	sec
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843	35	44.3	632	6	ABM35096	Human	sec	Abm35096	Human	sec	916	35	44.3	632	6	ABM01205	Human	sec	Abm01205	Human	sec
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847	35	44.3	632	6	ABO24618	Human	sec	AbO24618	Human	sec	920	35	44.3	632	6	ABO41974	Human	sec	AbO41974	Human	sec
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870	35	44.3	632	6	ABO16957	Human	sec	AbO16957	Human	sec	943	35	44.3	632	6	ABM34079	Human	sec	Abm34079	Human	sec
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872	35	44.3	632	6	ABR75889	Human	sec	AbR75889	Human	sec	945	35	44.3	632	6	ABO20315	Human	sec	AbO20315	Human	sec
873	35	44.3	632	6	ABR71265	Human	sec	AbR71265	Human	sec	946	35	44.3	632	6	ABO21230	Human	sec	AbO21230	Human	sec
874	35	44.3	632	6	ABR93162	Human	sec	AbR93162	Human	sec	947	35	44.3	632	6	ABO22145	Human	sec	AbO22145	Human	sec
875	35	44.3	632	6	ABR93467	Human	sec	AbR93467	Human	sec	948	35	44.3	632	6	ADA20074	Novel	hum	AdA20074	Novel	hum
876	35	44.3	632	6	ADA10203	Human	sec	AdA10203	Human	sec	949	35	44.3	632	6	ABO34186	Human	sec	AbO34186	Human	sec
877	35	44.3	632	6	ABR87892	Human	sec	AbR87892	Human	sec	950	35	44.3	632	6	ABR96579	Human	sec	AbR96579	Human	sec
878	35	44.3	632	6	ABO27892	Human	sec	AbO27892	Human	sec	951	35	44.3	632	6	ADA94435	Human	sec	AdA94435	Human	sec
879	35	44.3	632	6	ABO30027	Human	sec	AbO30027	Human	sec	952	35	44.3	632	6	ABR85757	Human	sec	AbR85757	Human	sec
880	35	44.3	632	6	ABO33236	Human	PRO	AbO33236	Human	PRO	953	35	44.3	632	6	ABR99739	Human	sec	AbR99739	Human	sec
881	35	44.3	632	6	ABM04924	Human	sec	Abm04924	Human	sec	954	35	44.3	632	6	ABM00290	Human	sec	Abm00290	Human	sec
882	35	44.3	632	6	ABM08884	Human	sec	Abm08884	Human	sec	955	35	44.3	632	6	ABM00595	Human	sec	Abm00595	Human	sec
883	35	44.3	632	6	ABO36484	Human	sec	AbO36484	Human	sec	956	35	44.3	632	6	ABO29722	Human	sec	AbO29722	Human	sec
884	35	44.3	632	6	ABO35569	Human	PRO	AbO35569	Human	PRO	957	35	44.3	632	6	ABM23588	Human	sec	Abm23588	Human	sec
885	35	44.3	632	6	ABO39534	Human	sec	AbO39534	Human	sec	958	35	44.3	632	6	ABM29383	Human	sec	Abm29383	Human	sec
886	35	44.3	632	6	ABM10409	Human	sec	Abm10409	Human	sec	959	35	44.3	632	6	ABO38314	Human	PRO	AbO38314	Human	PRO
887	35	44.3	632	6	ABM11934	Human	sec	Abm11934	Human	sec	960	35	44.3	632	6	ABO45614	Human	PRO	AbO45614	Human	PRO
888	35	44.3	632	6	ABO52080	Human	PRO	AbO52080	Human	PRO	961	35	44.3	632	6	ABM20538	Human	sec	Abm20538	Human	sec
889	35	44.3	632	6	ABO52385	Human	PRO	AbO52385	Human	PRO	962	35	44.3	632	6	ADA81437	Human	sec	AdA81437	Human	sec
890	35	44.3	632	6	ADA19902	Novel	hum	AdA19902	Novel	hum	963	35	44.3	632	6	ABO16652	Human	sec	AbO16652	Human	sec
891	35	44.3	632	6	ABO23703	Human	sec	AbO23703	Human	sec	964	35	44.3	632	6	ABO18278	Human	sec	AbO18278	Human	sec
892	35	44.3	632	6	ADB17285	Human	tra	AdB17285	Human	tra	965	35	44.3	632	6	ABO22705	Human	PRO	AbO22705	Human	PRO
893	35	44.3	632	6	ADA17747	Human	PRO	AdA17747	Human	PRO	966	35	44.3	632	6	ABO23010	Human	PRO	AbO23010	Human	PRO
894	35	44.3	632	6	ABR97189	Human	sec	AbR97189	Human	sec	967	35	44.3	632	6	ABR92552	Human	sec	AbR92552	Human	sec
895	35	44.3	632	6	ABR86977	Human	sec	AbR86977	Human	sec	968	35	44.3	632	6	ABR81509	Human	sec	AbR81509	Human	sec
896	35	44.3	632	6	ABM11019	Human	sec	Abm11019	Human	sec	969	35	44.3	632	6	ABM77933	Human	sec	Abm77933	Human	sec
897	35	44.3	632	6	ABM28163	Human	sec	Abm28163	Human	sec	970	35									

974 35 44.3 632 6 ABO30332 Human sec
975 35 44.3 632 6 ABM07359 Human sec
976 35 44.3 632 6 ABM03950 Human sec
977 35 44.3 632 6 ABO37094 Human sec
978 35 44.3 632 6 ABO41669 Human sec
979 35 44.3 632 6 ABO35264 Human PRO
980 35 44.3 632 6 ABM25113 Human sec
981 35 44.3 632 6 ABO47505 Human sec
982 35 44.3 632 6 ABO47810 Human sec
983 35 44.3 632 6 ABO48420 Human sec
984 35 44.3 632 6 ABO51470 Human PRO
985 35 44.3 632 6 ABO51775 Human PRO
986 35 44.3 632 6 ABO50555 Human sec
987 35 44.3 632 6 ABR79679 Human sec
988 35 44.3 632 6 ABM16941 Human sec
989 35 44.3 632 6 ABO17973 Human sec
990 35 44.3 632 6 ABO20925 Human sec
991 35 44.3 632 6 ABR96884 Human sec
992 35 44.3 632 6 ADA38660 Human sec
993 35 44.3 632 6 ABM12239 Human sec
994 35 44.3 632 6 ABM16331 Human sec
995 35 44.3 632 6 ABM24198 Human sec
996 35 44.3 632 6 ABM14679 Human sec
997 35 44.3 632 6 ABM04560 Human sec
998 35 44.3 632 6 ABM06749 Human sec
999 35 44.3 632 6 ABM09189 Human sec
1000 35 44.3 632 6 ABO39229 Human sec

ALIGNMENTS

RESULT 1
ID ABR61469 standard; peptide; 15 AA.
XX ABR61469;
XX
DT 01-SEP-2003 (first entry)
XX
DE Human disease specific marker CENP-E peptide.
XX
KW Human, biopolymer marker; disease state; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO2003045992-A1.
XX
PD 05-JUN-2003.
XX
PF 31-OCT-2002; 2002WO-CA001646.
XX
PR 23-NOV-2001; 2001US-00993399.
XX
PA (SYN-) SYN.X PHARMA INC.
XX
PI Jackowski G, Marshall J;
XX
DR WPI; 2003-505186/47.
XX
PT New biopolymer marker, useful for indicating, determining risk-assessment
PT of, or identifying therapeutic avenues related to, a disease state e.g.,
PT Alzheimer's disease.
XX
PS Claim 1; Page 41; 44pp; English.
XX
CC The invention relates to a novel biopolymer marker comprising a sequence
CC having 13 amino acids or its analyte, useful in indicating at least one
CC particular disease state. The biopolymer marker is useful for indicating,
CC determining risk-assessment of, or identifying therapeutic avenues
CC related to, a disease state e.g., Alzheimer's disease. The present
CC sequence represents the biopolymer marker of the invention

SQ Sequence 15 AA;
Query Match 100.0%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNNQRRSSRS 15
DB 1 RHYGETKNNQRRSSRS 15
|||||
RESULT 2
ID ADG89869 standard; protein; 355 AA.
XX
AC ADG89869;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human kinesin motor protein CENP-E340 SEQ ID NO:4.
XX
KW human; CENP-E; HsCENP-E; kinesin motor protein; CENP-E340; cytostatic;
KW neuroprotective; gene therapy; cellular proliferation disorder; cancer;
KW neurological disorder; vesicular transport disorder;
KW hyperproliferative cell growth disorder; centromere-associated protein.
XX
OS Homo sapiens.
XX
PN WO2003104426-A2.
XX
PD 18-DEC-2003.
XX
PF 09-JUN-2003; 2003WO-US018203.
XX
PR 10-JUN-2002; 2002US-0387403P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Harvey DM, Yang Y, Kohl NE;
XX
DR WPI; 2004-062347/06.
XX
DR N-PSDB; ADG89868.
XX
PT New centromere-associated motor protein, HsCENP-E, useful in diagnosing,
PT treating and preventing disorders characterized by excessive cellular
PT proliferation, including cancer, neurological disorders and disorders of
PT vesicular transport.
XX
PS Disclosure; SEQ ID NO 4; 108pp; English.
XX
CC The present sequence represents a human CENP-E (I) (HsCENP-E) which is a
CC kinesin motor protein, and a centromere-associated protein. The present
CC sequence is more specifically designated CENP-E340. Also described: (1) a
CC composition comprising (I) and a pharmaceutical excipient; (2) a method
CC for screening a compound as an agonist or antagonist of (I); (3) an
CC isolated and purified polynucleotide encoding (I), or which hybridises to
CC (I); (4) a method of detecting polynucleotide; (5) an expression vector
CC comprising the polynucleotide of (3); (6) a host cell comprising the
CC expression vector of (5); (7) a method for producing a polypeptide; (8) a
CC method of modulating cellular proliferation in a mammal; (9) a method of
CC inhibiting HsCENP-E mediated/induced cellular proliferation of a cell in
CC culture; and (10) a method of detecting the presence of cancer in an
CC individual. (I) has cytostatic and neuroprotective activities, and can be
CC used in gene therapy. The HsCENP-E protein can be used in screening
CC assays, in predictive medicine, e.g. diagnostic assays and
CC pharmacogenetics and in treating and preventing cancer, neurological
CC disorders and disorders of vesicular transport or useful in suppressing
CC hyperproliferative cell growth disorder.
XX
SQ Sequence 355 AA;
Query Match 100.0%; Score 79; DB 8; Length 355;

	Best Local Similarity	100.0%;	Pred. No.	1.9e-05;		Gaps	0;	
	Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;
Oy	1 RHYGETKNQRRSSRS	15						
Dd	189 RHYGETKNQRRSSRS	203						
RESULT 3								
ADV50412	ID ADV50412 standard; protein; 355 AA.							
XX AC	ADV50412;							
XX DT	10-MAR-2005 (first entry)							
XX XX	Human CENP-E kinesin motor domain.							
XX KW	ATPase modulator; CENP-E; kinesin; cell proliferation;							
KW KW	hyperproliferative disorders; cancer; breast tumor; restenosis;							
KW KW	cardiovascular disease; autoimmune disease; immune disorder; arthritis;							
KW KW	inflammation; musculoskeletal disease; graft rejection;							
KW KW	inflammatory bowel disease; gastrointestinal disease; cytostatic;							
KW KW	vasotropic; immunosuppressive; antiarthritic; antineoplastic;							
KW KW	gastrointestinal-gen.							
XX OS	Homo sapiens.							
XX PN	WO2004109290-A2.							
XX PD	16-DEC-2004.							
XX PF	28-MAY-2004; 2004WO-US017234.							
XX PP	30-MAY-2003; 2003US-0474488P.							
PR PR	03-JUN-2003; 2003US-0475873P.							
PR PR	17-MAR-2004; 2004US-0553838P.							
XX PA	(ROSE-) ROSETTA INPHARMATICS LLC.							
PA PI	(MERI) MERCK & CO INC.							
XX PI	Mao M, Linsley PS, Buser CA, Marshall CG, Kim AS;							
XX DR	WPI; 2005-057663/06.							
XX PT	Screening for modulators of target protein e.g., kinesin family 14							
PT PT	protein, by contacting target protein with candidate agent, and							
PT PT	determining whether candidate agent modulates activity of target protein.							
XX PS	Example 7; SEQ ID NO 19; 118pp; English.							
XX CC	The invention relates to a method (M1) of screening for modulators of a							
CC CC	target protein. The method involves contacting the target protein with							
CC CC	candidate agent, and determining whether the candidate agent modulates							
CC CC	activity of target protein, where the target protein comprises a sequence							
CC CC	that has more than 80% amino acid sequence identity to a fully defined							
CC CC	kinesin family 14 (KIF14) protein (SEQ ID No:2) or the KIF14 motor domain							
CC CC	sequence (SEQ ID No:3). Also described are: a method (M2) for modulating							
CC CC	cell proliferation, a method (M3) for treating a subject with a cellular							
CC CC	hyperproliferation disorder, a method (M4) for identifying candidate							
CC CC	subjects for treatment with an inhibitor of the activity of a target							
CC CC	protein, and a kit for screening for modulators of a target protein. A							
CC CC	cell viability assay, cell morphology assay, cell proliferation assay,							
CC CC	cell cycle distribution assay or apoptosis assay is used for determining							
CC CC	whether the candidate agent modulates the activity of the target protein.							
CC CC	The target protein comprises SEQ ID No:2, SEQ ID No:3, or a fragment of							
CC CC	SEQ ID No:3 having ATPase activity. The modulator is an inhibitor such as							
CC CC	RNA inhibitor, which is a KIF14 RNA inhibitor. The KIF14 RNA inhibitor							
CC CC	comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23							
CC CC	Method (M1) is useful for screening for modulators of a target protein,							
CC CC	particularly for screening modulators of Kif14 or Kif14 motor domain.							
CC CC	Method (M2) is useful for treating a subject with a cellular							
CC CC	hyperproliferation disorder such as cancer, preferably breast cancer.							

CC Method (M3) is useful for treating restenosis, autoimmune disease,
CC arthritis, graft rejection or inflammatory bowel disease. This sequence
CC represents human CENP-E kinesin motor domain.
XX
XX SQ Sequence 355 AA;

Query Match 100.0%; Score 79; DB 9; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps .0;

QY 1 RHYGETKMQRSSRS 15
|||||
DB 189 RHYGETKMQRSSRS 203

RESULT 4
ADG89867

ID ADG89867 standard; protein; 496 AA.
XX AC
XX ADG89867;
XX AC
XX DT 11-MAR-2004 (first entry)
XX DE
XX DE Human kinesin motor protein CENP-E465 SEQ ID NO:2.
XX KW human; CENP-E; HSCENP-E; kinesin motor protein; CENP-E465; cytostatic;
XX KW neuroprotective; gene therapy; cellular proliferation disorder; cancer;
XX KW neurological disorder; vesicular transport disorder;
XX KW hyperproliferative cell growth disorder; centromere-associated protein.
XX OS
XX OS Homo sapiens.
XX PN WO2003104426-A2.
XX PD
XX PD 18-DEC-2003.
XX PF
XX PF 09-JUN-2003; 2003WO-US018203.
XX PR
XX PR 10-JUN-2002; 2002US-0387403P.
XX PA (MERI) MERCK & CO INC.
XX PA Harvey DM, Yang Y, Kohl NE;
XX PI WPI; 2004-062347/06.
XX DR N-PSDB; ADG89866.
XX PT
XX PT New centromere-associated motor protein, HSCENP-E, useful in diagnosing,
XX PT treating and preventing disorders characterized by excessive cellular
XX PT proliferation, including cancer, neurological disorders and disorders of
XX PT vesicular transport.

Claim 1; SEQ ID NO 2; 108pp; English.

XX
XX The present sequence represents a human CENP-E (I) (HSCENP-E) which is a
XX CC kinesin motor protein, and a centromere-associated protein. The present
XX CC sequence is more specifically designated CENP-E465. Also described: (1) a
XX CC composition comprising (I) and a pharmaceutical excipient; (2) a method
XX CC for screening a compound as an agonist or antagonist of (I); (3) an
XX CC isolated and purified polynucleotide encoding (I), or which hybridises to
XX CC (I); (4) a method of detecting polynucleotide; (5) an expression vector
XX CC comprising the polynucleotide of (3); (6) a host cell comprising the
XX CC expression vector of (5); (7) a method for producing a polypeptide; (8) a
XX CC method of modulating cellular proliferation in a mammal; (9) a method of
XX CC inhibiting HSCENP-E mediated/induced cellular proliferation of a cell in
XX CC culture; and (10) a method of detecting the presence of cancer in an
XX CC individual. (I) has cytostatic and neuroprotective activities, and can be
XX CC used in gene therapy. The HSCENP-E protein can be used in screening
XX CC assays, in predictive medicine, e.g. diagnostic assays and
XX CC pharmacogenetics and in treating and preventing disorders characterised
XX CC by excessive cellular proliferation, including cancer, neurological
XX CC disorders and disorders of vesicular transport or useful in suppressing
XX CC hyperproliferative cell growth disorder.

XX Sequence 496 AA;
SQ Query Match 100.0%; Score 79; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.7e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNQSRSS 15
DB 189 RHYGETKNQSRSS 203
RESULT 5
ADW44257
ID ADW44257 standard; protein; 2503 AA.
XX ADW44257;
AC ADW44257;
XX 24-MAR-2005 (first entry)
DT Human centromere protein E variant 4 (CENPEv4).
DE
XX Drug screening; cell proliferation; proliferative disorder; cancer;
KW neoplasm; scleroderma; rheumatoid arthritis; musculoskeletal disease;
KW immune disorder; inflammation; cytostatic; dermatological; antiarthritic;
KW antirheumatic; centromere protein E; CENPE.
XX Homo sapiens.
OS
XX US2005003402-A1.
PN
XX 06-JAN-2005.
PD
XX 21-APR-2004; 2004US-00828985.
PF
XX 23-APR-2003; 2003US-0464905P.
PR 10-OCT-2003; 2003US-0510701P.
XX (ARMO//) ARMOUR C D.
PA (CAST//) CASTLE J C.
PA (GARR//) GARRETT-ENGELE P W.
PA (KANZ//) KAN Z.
PA (LOER//) LOERCH P M.
PA (TSIN//) TSINOREMAS N F.
XX Armour CD, Castle JC, Garrett-Englele PW, Kan Z, Loerch PM;
PI Tsinoremas NF;
PI WPI; 2005-065233/07.
XX N-PSDB; ADW44256.
DR
XX New nucleic acid encoding centromere protein E, useful for detecting
PT cancer and for inhibiting abnormal cell growth.
PT
XX Example 4; SEQ ID NO 11; 55pp; English.
PS
XX The invention relates to a novel splice isoform of human centromere
CC protein E (CENPE) designated CENPE variant 2 (CENPEv2, ADW44253) and to a
CC nucleic acid encoding it. Compared to CENPEv1 (REFSEQ NM 001813,
CC NP_001804), the CENPEv2 isoform lacks the sequence encoded by exon 38
CC (residues 1972-2066 of CENPEv1) and also has an Ala at position 300
CC instead of Pro. The invention also relates to an expression vector
CC comprising the CENPEv2 nucleic acid operably linked to an exogenous
CC promoter, and a method of screening for a compound able to bind to or
CC interact with CENPEv2 or a fragment thereof. The invention also discloses
CC other splice variants of CENPE designated CENPEv3 (lacking residues
CC encoded by exons 17 and 38 relative to CENPEv1) and CENPEv4 (lacking
CC residues encoded by exons 17, 18 and 38 relative to CENPEv1), and their
CC encoding nucleic acids. The CENPEv2 protein, nucleic acid and CENPEv2-
CC interacting compounds are useful in methods for inhibiting abnormal cell
CC proliferation and for detecting, treating or preventing cancer. As CENPE
CC has also been implicated in rheumatic disorders, CENPEv2-interacting
CC compounds may also be useful in treating or preventing disorders such as

CC systemic sclerosis and rheumatoid arthritis. The present sequence
CC represents the human CENPEv4 protein.
XX
SQ Sequence 2503 AA;
Query Match 100.0%; Score 79; DB 9; Length 2503;
Best Local Similarity 100.0%; Pred. No. 0.00016; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RHYGETKNQSRSS 15
DB 189 RHYGETKNQSRSS 203
RESULT 6
ADW44255
ID ADW44255 standard; protein; 2543 AA.
XX ADW44255;
AC ADW44255;
XX 24-MAR-2005 (first entry)
DT Human centromere protein E variant 3 (CENPEv3).
DE
XX Drug screening; cell proliferation; proliferative disorder; cancer;
KW neoplasm; scleroderma; rheumatoid arthritis; musculoskeletal disease;
KW immune disorder; inflammation; cytostatic; dermatological; antiarthritic;
KW antirheumatic; centromere protein E; CENPE.
XX Homo sapiens.
OS
XX US2005003402-A1.
PN
XX 06-JAN-2005.
PD
XX 21-APR-2004; 2004US-00828985.
PF
XX 23-APR-2003; 2003US-0464905P.
PR 10-OCT-2003; 2003US-0510701P.
XX (ARMO//) ARMOUR C D.
PA (CAST//) CASTLE J C.
PA (GARR//) GARRETT-ENGELE P W.
PA (KANZ//) KAN Z.
PA (LOER//) LOERCH P M.
PA (TSIN//) TSINOREMAS N F.
XX Armour CD, Castle JC, Garrett-Englele PW, Kan Z, Loerch PM;
PI Tsinoremas NF;
PI WPI; 2005-065233/07.
XX N-PSDB; ADW44254.
DR
XX New nucleic acid encoding centromere protein E, useful for detecting
PT cancer and for inhibiting abnormal cell growth.
PT
XX Example 4; SEQ ID NO 9; 55pp; English.
PS
XX The invention relates to a novel splice isoform of human centromere
CC protein E (CENPE) designated CENPE variant 2 (CENPEv2, ADW44253) and to a
CC nucleic acid encoding it. Compared to CENPEv1 (REFSEQ NM 001813,
CC NP_001804), the CENPEv2 isoform lacks the sequence encoded by exon 38
CC (residues 1972-2066 of CENPEv1) and also has an Ala at position 300
CC instead of Pro. The invention also relates to an expression vector
CC comprising the CENPEv2 nucleic acid operably linked to an exogenous
CC promoter, and a method of screening for a compound able to bind to or
CC interact with CENPEv2 or a fragment thereof. The invention also discloses
CC other splice variants of CENPE designated CENPEv3 (lacking residues
CC encoded by exons 17 and 38 relative to CENPEv1) and CENPEv4 (lacking
CC residues encoded by exons 17, 18 and 38 relative to CENPEv1), and their
CC encoding nucleic acids. The CENPEv2 protein, nucleic acid and CENPEv2-
CC interacting compounds are useful in methods for inhibiting abnormal cell
CC proliferation and for detecting, treating or preventing cancer. As CENPE
CC has also been implicated in rheumatic disorders, CENPEv2-interacting
CC compounds may also be useful in treating or preventing disorders such as

CC has also been implicated in rheumatic disorders, CENPEV2-interacting
 CC compounds may also be useful in treating or preventing disorders such as
 CC systemic sclerosis and rheumatoid arthritis. The present sequence
 CC represents the human CENPEV3 protein.

XX Sequence 2543 AA;
 SQ Query Match 100.0%; Score 79; DB 9; Length 2543;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
 |||||
 Db 189 RHYGETKNQSRSSRS 203

RESULT 7
 ADW44253
 ID ADW44253 standard; protein; 2568 AA.
 XX AC ADW44253;
 XX DT 24-MAR-2005 (first entry)
 XX DE Human centromere protein E variant 2 (CENPEV2).
 XX KW Drug screening; cell proliferation; proliferative disorder; cancer;
 KW neoplasm; scleroderma; rheumatoid arthritis; musculoskeletal disease;
 KW immune disorder; inflammation; cytostatic; dermatological; antiarthritic;
 KW antirheumatic; centromere protein E; CENPE.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1971..1972
 FT /note= "These residues correspond to the exon 37-exon 39
 FT junction. The corresponding residues in CENPEV1 (residues
 FT 1971 and 2067) are separated by 95 amino acids encoded by
 FT exon 38 (SEQ ID NO:19)"
 XX US2005003402-A1.
 PN 06-JAN-2005.
 PD 21-APR-2004; 2004US-00828985.
 XX 23-APR-2003; 2003US-0464905P.
 PR 10-OCT-2003; 2003US-0510701P.
 XX (ARMO/) ARMOUR C D.
 PA (CAST/) CASTLE J C.
 PA (GARR/) GARRETT-ENGELE P W.
 PA (KANZ/) KAN Z.
 PA (LOER/) LOERCH P M.
 PA (TSIN/) TSINOREMAS N F.
 XX Armour CD, Castle JC, Garrett-Engle PW, Kan Z, Loerch PM;
 PI Tsinoremas NF;
 XX WPI: 2005-065233/07.
 DR N-PSDB; ADW44252.
 XX New nucleic acid encoding centromere protein E, useful for detecting
 PT cancer and for inhibiting abnormal cell growth.
 PS Claim 4; SEQ ID NO 7; 55pp; English.
 XX The invention relates to a novel splice isoform of human centromere
 CC protein E (CENPE) designated CENPE variant 2 (CENPEV2, ADW44253) and to a
 CC nucleic acid encoding it. Compared to CENPEV1 (REFSEQ NM_001813,
 CC NP_001804), the CENPEV2 isoform lacks the sequence encoded by exon 38
 CC (residues 1972-2066 of CENPEV1) and also has an Ala at position 300
 CC instead of Pro. The invention also relates to an expression vector

CC comprising the CENPEV2 nucleic acid operably linked to an exogenous
 CC promoter, and a method of screening for a compound able to bind to or
 CC interact with CENPEV2 or a fragment thereof. The invention also discloses
 CC other splice variants of CENPE designated CENPEV3 (lacking residues
 CC encoded by exons 17 and 38 relative to CENPEV1) and CENPEV4 (lacking
 CC residues encoded by exons 17, 18 and 38 relative to CENPEV1), and their
 CC encoding nucleic acids. The CENPEV2 protein, nucleic acid and CENPEV2-
 CC interacting compounds are useful in methods for inhibiting abnormal cell
 CC proliferation and for detecting, treating or preventing cancer. As CENPE
 CC has also been implicated in rheumatic disorders, CENPEV2-interacting
 CC compounds may also be useful in treating or preventing disorders such as
 CC systemic sclerosis and rheumatoid arthritis. The present sequence
 CC represents the specifically claimed human CENPEV2 protein.

XX Sequence 2568 AA;
 SQ Query Match 100.0%; Score 79; DB 9; Length 2568;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
 |||||
 Db 189 RHYGETKNQSRSSRS 203

RESULT 8
 ABG06505
 ID ABG06505 standard; protein; 2633 AA.
 XX AC ABG06505;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #6496.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX WPI: 2001-639362/73.
 DR N-PSDB; AAS70692.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 36864; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 2633 AA;
 Query Match 100.0%; Score 79; DB 4; Length 2633;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 |||||
 Db 189 RHYGETKMNQSRSS 203
 |||||
 RESULT 9
 AAM39097
 ID AAM39097 standard; protein; 2663 AA.
 AC AAM39097;
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 2242.
 XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS
 XX WO200153312-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 26-DEC-2000; 2000WO-US034263.
 PF
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI58253.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 PT
 XX Example 4; SEQ ID NO 2242; 10078pp; English.
 PS
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the

CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, drug screening,
 CC and thrombolytic activity, cancer diagnosis and therapy, leukaemias and
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 XX SQ Sequence 2663 AA;
 Query Match 100.0%; Score 79; DB 4; Length 2663;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 |||||
 Db 189 RHYGETKMNQSRSS 203
 |||||
 RESULT 10
 ADQ17932
 ID ADQ17932 standard; protein; 2663 AA.
 XX ADQ17932;
 AC ADQ17932;
 DT 26-AUG-2004 (first entry)
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 749.
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KW
 XX Homo sapiens.
 OS
 XX WO2004048938-A2.
 PN
 XX 10-JUN-2004.
 PD
 XX 26-NOV-2003; 2003WO-US038193.
 PF
 XX 26-NOV-2002; 2002US-0429739P.
 PR
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA
 XX Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI; 2004-441208/41.
 DR
 XX Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 XX Example 2; SEQ ID NO 749; 210pp; English.
 PS
 XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 2663 AA;

Query Match 100.0%; Score 79; DB 8; Length 2663;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 |||||
 DB 189 RHYGETKNQSRSS 203

RESULT 11
 ADX06867
 ID ADX06867 standard; protein; 2663 AA.
 AC ADX06867;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1432.
 XX
 KW cytotatic; cyclin-dependent kinase; cdk; biomarker.
 XX
 OS Homo sapiens.
 XX
 PN WO2005012875-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 29-JUL-2004; 2004WO-US024424.
 XX
 PR 29-JUL-2003; 2003US-0490890P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 XX
 DR WPI; 2005-163068/17.
 DR N-PSDB; ADX06866.
 XX

PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.

PS Claim 5; SEQ ID NO 1432; 141pp; English.

CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed
 CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylthyl)-2-
 CC oxazolyl]methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
 CC sequence represents a biomarker used in the method of the invention.

SQ Sequence 2663 AA;

Query Match 100.0%; Score 79; DB 9; Length 2663;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 |||||
 DB 189 RHYGETKNQSRSS 203

RESULT 12
 AAM40883
 ID AAM40883 standard; protein; 2688 AA.
 AC AAM40883;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 5814.

XX Human; nootropic; immunosuppressant; cytotatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.
 OS
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX

XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-0052317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.
 DR N-PSDB; AAI60039.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 as central nervous system injuries.

PS Example 2; SEQ ID NO 5814; 10078pp; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytotatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression.
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 2688 AA;

SQ

Mon Apr 24 09:14:16 2006

Query Match 100.0%; Score 79; DB 4; Length 2688;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | |
DB 213 RHYGETKNQRRSSRS 227

RESULT 13
ID AAY01632 standard; protein; 2954 AA.
AC AAY01632;
XX
DT 22-JUN-1999 (first entry)
XX
DE Amino acid sequence of centromere-associated protein-E (CENP-E).
XX
KW CENP-E; centromere-associated protein-E; ATPase activity;
KW plus end-directed microtubule motor activity; chromosome congression;
KW microtubule binding activity; chromosome movement; mitosis;
KW cell proliferation; tumor; metastasis; vascular malfunction;
KW inflammatory disease; immune disease; angiogenesis; hypertension;
KW restenosis; fungal infection; selective herbicide; fungicide;
KW insecticide; plant growth regulator; activator; cancer cell marker.
XX
OS Xenopus sp.
XX
PN WO9913061-AL.
XX
PD 18-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US019231.
XX
PR 11-SEP-1997; 97US-0058645P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Wood KW, Sakowicz R, Goldstein LSB, Cleveland DW;
XX
XX WPI; 1999-229233/19.
XX
XX N-PSDB; AAX46819.
XX
XX Centromere-associated protein-E and related nucleic acid.
XX
XX Claim 5; Page 66-67; 77pp; English.
XX
XX The present sequence represents CENP-E (centromere-associated protein-E)
XX of Xenopus. The protein has at least one of plus end-directed microtubule
XX motor activity, ATPase (adenosine triphosphatase) activity and
XX microtubule binding activity. CENP-E is the motor that powers chromosome
XX movement toward microtubule plus ends and is essential for congression of
XX chromosomes during mitosis. Modulators of CENP-E can thus control cell
XX proliferation. Agents that modulate CENP-E activity are lead therapeutic,
XX biocultural and diagnostic agents, e.g. for treatment of unwanted
XX cell proliferation (typical of many examples are tumors and metastases;
XX vascular malfunction; inflammatory and immune diseases; angiogenesis;
XX hypertension; restenosis; and fungal infections), also as plant-
XX protection agents (selective herbicides, fungicides and insecticides) and
XX plant growth regulators or activators for improving yields. CENP-E is
XX also a diagnostic marker for dividing cells, including cancer cells
XX
XX Sequence 2954 AA;

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
| | | | | | | | | | | | | | |
DB 187 RHYGETKNQRRSSRS 201

RESULT 14
ID ADX97061 standard; protein; 694 AA.
XX
AC ADX97061;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 59725.
XX

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PR 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 59725; 15pp; English.
XX

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for increasing the rate of homologous
XX lignin or plant growth regulators, for increasing the rate of modification of
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 694 AA;

Query Match 82.3%; Score 65; DB 8; Length 694;
Best Local Similarity 80.0%; Pred. No. 0.012;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
 DB 221 RHFGETNMRRSRS 235

RESULT 15
 AAR57365
 ID AAR57365 standard; protein; 955 AA.
 XX AC AAR57365;
 XX DT 16-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 08-MAR-1995 (first entry)
 DE K39 polypeptide of Leishmania chagasi.
 KW Parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
 KW Leishmania chagasi.
 XX OS Leishmania donovani chagasi.
 XX PN WO9416331-A1.
 XX PD 21-JUL-1994.
 XX PF 10-JAN-1994; 94WO-US000324.
 XX PR 15-JAN-1993; 93US-00006676.
 XX PA (IASY-) IASYS CORP.
 XX PI Reed SG;
 XX WPI; 1994-249402/30.
 XX N-PSDB; RAQ70152.
 XX Diagnosis of Leishmaniasis - by determining the presence of antibodies
 PT that bind to a K39 repeat unit antigen.
 XX Disclosure; Page 12-15; 28pp; English.
 CC The K39 polypeptide comprises a number of repeated units (described in
 CC AAR57366). Detection of antibodies directed against this repeated unit in
 CC a patients sample is indicative of leishmaniasis. The antigenic repeat
 CC unit can itself be used as a vaccine to protect against infection by a
 CC leishmania parasite. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 16-OCT-2003 to standardise OS field)

QY 1 RHYGETKNQRRSRS 15
 DB 241 RHTASTKNQRRSRS 255

RESULT 16
 AAW03691
 ID AAW03691 standard; protein; 955 AA.
 XX AC AAW03691;
 XX DT 16-OCT-2003 (revised)
 XX DT 09-MAR-1997 (first entry)
 DE Leishmania chagasi K39 antigen.
 XX Leishmania chagasi; acidic ribosomal antigen; LcP0; epitope; K39.

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.6;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX Leishmania donovani chagasi.
 XX WO9633414-A2.
 XX PD 24-OCT-1996.
 XX PF 19-APR-1996; 96WO-US005472.
 XX PR 21-APR-1995; 95US-00428414.
 XX PA (CORI-) CORIXA CORP.
 XX PI Reed SG;
 XX WPI; 1996-485884/48.
 XX N-PSDB; AAT42166.
 XX New Leishmania acidic ribosomal P-protein family polypeptide - used to
 PT develop prods. for diagnosis, detection and protection against Leishmania
 PT infections.
 XX Disclosure; Page 36-43; 76pp; English.
 CC Compounds including polypeptides that contain at least an epitope of the
 CC i. chagasi acidic ribosomal antigen LcP0 are useful in a variety of
 CC immunoassays for detecting Leishmania infection. Portions of LcP0
 CC (AAT42164) contg. at least the 17 C-terminal amino acids (AAT42165) have
 CC been found to generate a signal in an ELISA that is equivalent to that
 CC generated by the full length LcP0. A combination polypeptide may also be
 CC used, comprising an LcP0 epitope along with an epitope derived from the
 CC Leishmania K39 antigen (AAT42166), pref. the K39 repeat unit antigen
 CC having the sequence given in AAW03690. (Updated on 16-OCT-2003 to
 CC standardise OS field)

QY 1 RHYGETKNQRRSRS 15
 DB 241 RHTASTKNQRRSRS 255

RESULT 17
 ABB62322
 ID ABB62322 standard; protein; 2013 AA.
 XX AC ABB62322;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 13758.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 1.6;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX WPI; 2001-656860/75.
DR N-PSDB; ABL06425.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 13759; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABU01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2013 AA;
Query Match 67.1%; Score 53; DB 4; Length 2013;
Best Local Similarity 73.3%; Pred. No. 5.3;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETQNRSSRS 15
DB 183 RTVGETNMRSSRS 197
RESULT 18
AAB40661
ID AAB40661 standard; protein; 154 AA.
XX
XX AAB40661;
AC
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF425 polypeptide sequence SEQ ID NO:850.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
XX WO200058473-A2.
PN
XX 05-OCT-2000.
PD
XX 31-MAR-2000; 2000WO-US008621.
PF
XX 31-MAR-1999; 99US-0127607P.
PR
XX 02-APR-1999; 99US-0127636P.
PR
XX 05-APR-1999; 99US-0127728P.
PR
XX 30-MAR-2000; 2000US-00540763.
PR
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI

XX WPI; 2000-602162/57.
DR N-PSDB; AAC74870.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 11; Page 888-889; 5507pp; English.
PS
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 154 AA;
Query Match 65.8%; Score 52; DB 3; Length 154;
Best Local Similarity 66.7%; Pred. No. 0.49;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETQNRSSRS 15
DB 29 RHTGTQWNEHSRS 43
RESULT 19
ABP31636
ID ABP31636 standard; protein; 154 AA.
XX
XX ABP31636;
AC
XX
DT 09-JUL-2002 (first entry)
DE Human structural protein-like ORF609 protein, SEQ ID NO:1218.
XX
KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnary;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide.
XX
OS Homo sapiens.
XX
XX WO200190366-A2.
PN
XX 29-NOV-2001.
PD
XX 24-MAY-2001; 2001WO-US017076.
PF

XX 24-MAY-2000; 2000US-0206690P.
 XX (CURA-) CURAGEN CORP.
 XX Leach MD, Shimkets RA;
 XX WPI; 2002-106200/14.
 XX N-PSDB; ABN75662.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation.
 XX Claim 10; Page 570; 2508pp; English.
 XX Sequences ABP31028-ABP3561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases
 XX
 XX Sequence 154 AA;
 SQ
 Query Match 65.8%; Score 52; DB 5; Length 154;
 Best Local Similarity 66.7%; Pred. No. 0.49;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGKTKNQRRSSRS 15
 ||| ||| ||| |||
 Db 29 RHTGTTQMNHSRS 43
 RESULT 20
 ABB80079
 ID ABB80079 standard; protein; 341 AA.
 XX
 AC ABB80079;
 XX
 XX 27-AUG-2002 (first entry)
 DT
 DE Human kinesin motor protein (HsKrp5) motor domain amino acid sequence.
 XX

KW Human; kinesin motor protein; HsKrp5; cytostatic; cardiovascular;
 KW immunomodulatory; anti-inflammatory; vaccine; gene therapy;
 KW spindle morphogenesis; chromosome; cell division;
 KW cellular proliferation disorder; cancer; hyperplasias; restenosis;
 KW cardiac hypertrophy; immune disorder; inflammation.
 XX Homo sapiens.
 XX US6379941-B1.
 XX 30-APR-2002.
 XX 27-NOV-2000; 2000US-00724517.
 XX 17-AUG-2000; 2000US-00641807.
 XX (CYTO-) CYTOKINETICS INC.
 XX Beraud C, Freedman R;
 XX WPI; 2002-413719/44.
 XX Isolated human Kinesin motor protein HsKrp5, useful for preventing,
 PT diagnosing and treating e.g. cancer, hyperplasias, restenosis, cardiac
 PT hypertrophy, immune disorders and inflammation.
 XX Claim 4; Fig 4; 29pp; English.
 XX The invention relates to an isolated human Kinesin motor protein
 CC (HsKrp5). The activity of the protein of the invention may be described
 CC as cytostatic, cardiovascular, immunomodulatory and anti-inflammatory.
 CC The protein may be used in a vaccine or in gene therapy. Kinesin-related
 CC proteins (KRPs) participate in spindle morphogenesis and chromosome
 CC movement in cell division. The anti-HsKrp5 agonists, antibodies and
 CC antagonists may be used to regulate HsKrp5 expression and activity. The
 CC anti-HsKrp5 antibodies may also be used as diagnostic agents for
 CC detecting the presence of HsKrp5 in samples (e.g. by enzyme linked
 CC immunosorbant assay (ELISA)) and therefore diagnose diseases associated
 CC with aberrant HsKrp5 expression and activity. They may be used in this
 CC way to prevent, diagnose and treat cellular proliferation disorders e.g.
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation. The current sequence represents the human kinesin motor
 CC protein (HsKrp5) motor domain amino acid sequence
 XX Sequence 341 AA;
 SQ
 Query Match 65.8%; Score 52; DB 5; Length 341;
 Best Local Similarity 66.7%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGKTKNQRRSSRS 15
 ||| ||| ||| |||
 Db 192 RHTGTTQMNHSRS 206
 RESULT 21
 ABBG72398
 ID ABBG72398 standard; protein; 341 AA.
 XX
 AC ABBG72398;
 XX
 XX 11-FEB-2003 (first entry)
 DT
 DE Human kinesin protein, HsKrp5, motor domain.
 XX
 KW Human; kinesin; HsKrp5; ATPase; microtubule; cellular proliferation;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; autoimmune disease;
 KW immune disorder; arthritis; graft rejection; inflammatory bowel disease;
 KW inflammation; neurological disorder; vesicular transport disorder;
 KW enzyme; motor domain.
 XX Homo sapiens.
 XX

PN US6448026-B1.
 XX 10-SEP-2002.
 XX 27-NOV-2000; 2000US-00723096.
 XX 17-AUG-2000; 2000US-00641807.
 XX (CYTO-) CYTOKINETICS INC.
 XX Beraud C, Freedman R;
 XX WPI; 2003-089119/08.
 XX N-PSDB; ABX13614.
 XX Screening for modulators of human kinesin protein HsKrp5, which are
 PT useful in treating cancers or restenosis, comprises detecting binding or
 PT ATPase activity levels of the protein in a first and second concentration
 PT of a candidate agent.
 XX Claim 8; Fig 4; 30pp; English.
 XX The invention relates to screening for modulators of a target protein,
 CC comprises detecting the level of binding activity or ATPase activity of
 CC the target protein when contacted with a first and second concentration
 CC of a candidate agent. The target protein comprises a sequence that has
 CC greater than 90% amino acid identity with a sequence of human kinesin
 CC protein HsKrp5 (or its motor domain). The method is useful for screening
 CC for modulators of a target protein having microtubule stimulated ATPase
 CC activity, particularly the human kinesin protein HsKrp5. The modulators
 CC of HsKrp5 are useful in diagnosing, preventing or treating cellular
 CC proliferation (e.g. cancers (many examples given in the specification) or
 CC hyperplasia), restenosis, cardiac hypertrophy, autoimmune disease, immune
 CC disorders, arthritis, graft rejection, inflammatory bowel disease,
 CC inflammation, neurological disorders, or disorders of vesicular
 CC transport. The present sequence represents human HsKrp5, motor domain
 XX Sequence 341 AA;
 SQ Query Match 65.8%; Score 52; DB 6; Length 341;
 Best Local Similarity 66.7%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 DB 192 RHTGTTQMNEHSRS 206
 RESULT 22
 ABR44339
 ID ABR44339 standard; protein; 348 AA.
 XX ABR44339;
 XX 11-AUG-2003 (first entry)
 XX Polypeptide-kinesin-38.28.
 XX Polypeptide-kinesin-38.28; paralysis; arrhythmia; bronchial asthma;
 KW peptic ulcer.
 XX Unidentified.
 OS CN1380331-A.
 PN 20-NOV-2002.
 PD 10-APR-2001; 2001CN-00105929.
 PF 10-APR-2001; 2001CN-00105929.
 XX (SHAN-) SHANGHAI BIONOW GENE DEV INC.
 PA

PI Mao Y, Xie Y;
 XX WPI; 2003-222563/22.
 DR N-PSDB; ACC00158.
 XX Polypeptide-kinesin-38.28 and polynucleotide for coding this polypeptide.
 XX Claim 1; Page 28-29; 32pp; Chinese.
 XX The present invention discloses a polypeptide-kinesin-38.28, The
 CC invention also discloses the method for curing several diseases, such as
 CC paralysis, arrhythmia, bronchial asthma, peptic ulcer and dementia by
 CC using the polypeptide. The present sequence represents kinesin 38.28
 XX Sequence 348 AA;
 SQ Query Match 65.8%; Score 52; DB 6; Length 348;
 Best Local Similarity 66.7%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQSRSS 15
 DB 11 RHTGTTQMNEHSRS 25
 RESULT 23
 ABB80078
 ID ABB80078 standard; protein; 1279 AA.
 XX ABB80078;
 AC 27-AUG-2002 (first entry)
 XX Human kinesin motor protein (HsKrp5) amino acid sequence.
 DE Human; kinesin motor protein; HsKrp5; cytostatic; cardiovascular;
 KW immunomodulatory; anti-inflammatory; vaccine; gene therapy;
 KW spindle morphogenesis; chromosome; cell division;
 KW cellular proliferation disorder; cancer; hyperplasias; restenosis;
 KW cardiac hypertrophy; immune disorder; inflammation.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 409..446
 FT /label= Xaa
 FT /note= "Xaa may be any amino acid"
 XX US6379941-B1.
 XX 30-APR-2002.
 XX 27-NOV-2000; 2000US-00724517.
 XX 17-AUG-2000; 2000US-00641807.
 XX (CYTO-) CYTOKINETICS INC.
 XX Beraud C, Freedman R;
 XX WPI; 2002-413719/44.
 XX N-PSDB; ABL58668.
 XX Isolated human kinesin motor protein HsKrp5, useful for preventing,
 PT diagnosing and treating e.g. cancer, hyperplasias, restenosis, cardiac
 PT hypertrophy, immune disorders and inflammation.
 XX Claim 4; Fig 2; 29pp; English.
 XX The invention relates to an isolated human kinesin motor protein
 CC (HsKrp5). The activity of the protein of the invention may be described
 CC as cytostatic, cardiovascular, immunomodulatory and anti-inflammatory.
 CC The protein may be used in a vaccine or in gene therapy. Kinesin-related

CC proteins (KRP5) participate in spindle morphogenesis and chromosome
 CC movement in cell division. The anti-Hskrp5 agonists, antibodies and
 CC antagonists may be used to regulate Hskrp5 expression and activity. The
 CC anti- Hskrp5 antibodies may also be used as diagnostic agents for
 CC detecting the presence of Hskrp5 in samples (e.g. by enzyme linked
 CC immunosorbant assay (ELISA)) and therefore diagnose diseases associated
 CC with aberrant Hskrp5 expression and activity. They may be used in this
 CC way to prevent, diagnose and treat cellular proliferation disorders e.g.
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation. The current sequence represents the human kinesin motor
 CC protein (Hskrp5) amino acid sequence
 XX
 SQ Sequence 1279 AA;

Query Match 65.8%; Score 52; DB 5; Length 1279;
 Best Local Similarity 66.7%; Pred. No. 4.9;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHVGETKMNQSRSS 15
 |||:|:|:|:|
 Db 194 RHTGTTQMNEHSRS 208

RESULT 24
 ABG70787
 ID ABG70787 standard; protein; 1279 AA.
 XX
 AC ABG70787;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human kinesin-related protein 5 (Hskrp5) protein.
 XX
 KW Human; kinesin-related protein 5; Hskrp5; motor protein; microtubule;
 KW ATPase activity; Krp; spindle morphogenesis; chromosome movement;
 KW cell division; diagnostic; therapeutic; biopsied tissue; cancer; tumour;
 KW psoriasis; keloid; neurological disorder; autoimmune disease; arthritis;
 KW graft rejection; inflammatory bowel disease; vesicular transport;
 KW antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 3..343
 FT /label= Motor domain
 FT /note= "This domain is specifically claimed in claim 3"
 FT Misc-difference 409..446
 FT /label= Unknown
 FT /note= "Residues are not defined in the specification"

XX
 PN US6440731-B1.
 XX
 XX 27-AUG-2002.
 XX
 PF 17-AUG-2000; 2000US-00641807.
 XX
 PR 17-AUG-2000; 2000US-00641807.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C, Freedman R;
 XX
 DR WPI; 2002-739590/80.
 DR N-PSDB; ABS4500.
 XX
 XX Novel isolated nucleic acid sequence encoding a motor protein, useful for
 PT diagnosing, preventing and treating cancer, psoriasis, keloids,
 PT neurological disorders and disorders of vesicular transport.
 XX
 PS Claim 3; Fig 2; 30pp; English.
 XX
 CC The invention discloses an isolated nucleic acid which encodes a human
 CC kinesin-related motor protein (Hskrp5) that has a microtubule stimulated

CC ATPase activity. Krps participate in spindle morphogenesis and chromosome
 CC movement in cell division. The Hskrp5 nucleic acid is useful for
 CC diagnostic purposes to determine the presence, or absence, and excess
 CC expression of Hskrp5 and to monitor the regulation of Hskrp5 levels
 CC during therapeutic intervention. The nucleic acid is also useful to
 CC detect and quantitate gene expression in biopsied tissues in which Hskrp5
 CC may be correlated with the disease and in assays to detect the presence
 CC of associated disorders. The nucleic acid and its encoded protein are
 CC useful in diagnosing, preventing and treating cancer, tumours, psoriasis,
 CC keloids, neurological disorders, autoimmune disease, arthritis, graft
 CC rejection, inflammatory bowel disease and disorders of vesicular
 CC transport. The sequence presented is the human Hskrp5 protein
 XX
 SQ Sequence 1279 AA;

Query Match 65.8%; Score 52; DB 5; Length 1279;
 Best Local Similarity 66.7%; Pred. No. 4.9;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHVGETKMNQSRSS 15
 |||:|:|:|:|
 Db 194 RHTGTTQMNEHSRS 208

RESULT 25
 ABG72397
 ID ABG72397 standard; protein; 1279 AA.
 XX
 AC ABG72397;
 XX
 DT 11-FEB-2003 (first entry)
 XX
 DE Human partial kinesin protein, Hskrp5.
 XX
 KW Human; kinesin; Hskrp5; ATPase; microtubule; cellular proliferation;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; autoimmune disease;
 KW immune disorder; arthritis; graft rejection; inflammatory bowel disease;
 KW inflammation; neurological disorder; vesicular transport disorder;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 409
 FT /label= UNKNOWN
 FT /note= "Encoded by TNN"
 FT Misc-difference 410..445
 FT /label= UNKNOWN
 FT /note= "Encoded by nucleotides 1336-1339 of the DNA
 FT sequence appearing as ABX13613"
 FT Misc-difference 446
 FT /label= UNKNOWN
 FT /note= "Encoded by NGA"

XX
 PN US6448026-B1.
 XX
 PD 10-SEP-2002.
 XX
 PF 27-NOV-2000; 2000US-00723096.
 XX
 PR 17-AUG-2000; 2000US-00641807.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C, Freedman R;
 XX
 DR WPI; 2003-089119/08.
 DR N-PSDB; ABX13613.
 XX
 PT Screening for modulators of human kinesin protein Hskrp5, which are
 PT useful in treating cancers or restenosis, comprises detecting binding or
 PT ATPase activity levels of the protein in a first and second concentration
 PT of a candidate agent.

XX Claim 5; Fig 2; 30pp; English.

XX The invention relates to screening for modulators of a target protein,

CC comprises detecting the level of binding activity or ATPase activity of

CC the target protein when contacted with a first and second concentration

CC of a candidate agent. The target protein comprises a sequence that has

CC greater than 90% amino acid identity with a sequence of human kinesin

CC protein HsKrp5 (or its motor domain). The method is useful for screening

CC for modulators of a target protein having microtubule stimulated ATPase

CC activity, particularly the human kinesin protein HsKrp5. The modulators

CC of HsKrp5 are useful in diagnosing, preventing or treating cellular

CC proliferation (e.g. cancers (many examples given in the specification) or

CC hyperplasia), restenosis, cardiac hypertrophy, autoimmune disease, immune

CC disorders, arthritis, graft rejection, inflammatory bowel disease,

CC inflammation, neurological disorders, or disorders of vesicular

CC transport. The present sequence represents human HsKrp5

XX

XX Sequence 1279 AA;

Query Match 65.8%; Score 52; DB 6; Length 1279;

Best Local Similarity 66.7%; Pred. No. 4.9;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETQNRSSRS 15

DB 194 RHTGTTQNRSSRS 208

RESULT 26

ADJ94914

ID ADJ94914 standard; protein; 1401 AA.

XX

AC ADJ94914;

XX

DT 06-MAY-2004 (first entry)

XX

DE Novel NOVX protein sequence #71.

XX

KW antidiabetic; anorectic; cardiac; hypotensive; antiarteriosclerotic;

KW anorectic; viricide; antibacterial; fungicide; protozoicide; nootropic;

KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;

KW antirheumatic; antiinflammatory; dermatological; antiasthmatic;

KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;

KW infectious disease; anorexia; cancer; cardiovascular disease;

KW hypertension; atherosclerosis; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;

KW osteoarthritis; hematopoietic disorder; inflammatory skin disorder;

KW asthma; dyslipidemia; neurogenesis; cell differentiation;

KW cell proliferation; hematopoiesis; wound healing; angiogenesis;

KW chromosome mapping; tissue typing; pharmacogenomic.

XX

OS Homo sapiens.

XX

PN WO2003040325-A2.

XX

PD 15-MAY-2003.

XX

XX 05-NOV-2002; 2002WO-US035464.

XX

XX 05-NOV-2001; 2001US-0338626P.

XX

PR 06-NOV-2001; 2001US-0333072P.

PR

PR 09-NOV-2001; 2001US-0348283P.

PR

PR 15-NOV-2001; 2001US-0335610P.

PR

PR 16-NOV-2001; 2001US-0338543P.

PR

PR 20-NOV-2001; 2001US-0331630P.

PR

PR 21-NOV-2001; 2001US-0331641P.

PR

PR 27-NOV-2001; 2001US-0332152P.

PR

PR 28-NOV-2001; 2001US-0333461P.

PR

PR 28-NOV-2001; 2001US-0333912P.

PR

PR 29-NOV-2001; 2001US-0334027P.

PR

PR 30-NOV-2001; 2001US-0334300P.

PR

PR 30-NOV-2001; 2001US-0334421P.

PR

30-NOV-2001; 2001US-0334526P.

PR

04-DEC-2001; 2001US-0336576P.

PR

04-DEC-2001; 2001US-033664P.

PR

07-DEC-2001; 2001US-0338114P.

PR

10-DEC-2001; 2001US-0338390P.

PR

10-DEC-2001; 2001US-0339006P.

PR

11-DEC-2001; 2001US-0339008P.

PR

01-FEB-2002; 2002US-0339286P.

PR

01-FEB-2002; 2002US-0353280P.

PR

01-FEB-2002; 2002US-0353288P.

PR

04-FEB-2002; 2002US-0354392P.

PR

04-FEB-2002; 2002US-0354393P.

PR

04-FEB-2002; 2002US-0354409P.

PR

27-FEB-2002; 2002US-035944P.

PR

05-MAR-2002; 2002US-0361790P.

PR

05-MAR-2002; 2002US-0361833P.

PR

05-MAR-2002; 2002US-0361925P.

PR

05-MAR-2002; 2002US-0362230P.

PR

05-MAR-2002; 2002US-0362625P.

PR

13-MAR-2002; 2002US-0364000P.

PR

13-MAR-2002; 2002US-0364181P.

PR

13-MAR-2002; 2002US-0364182P.

PR

13-MAR-2002; 2002US-0364197P.

PR

13-MAR-2002; 2002US-0364227P.

PR

28-MAY-2002; 2002US-0381621P.

PR

17-JUL-2002; 2002US-0396703P.

PR

06-AUG-2002; 2002US-0401552P.

PR

07-AUG-2002; 2002US-0401594P.

PR

07-AUG-2002; 2002US-0401787P.

PR

15-AUG-2002; 2002US-0403619P.

PR

20-AUG-2002; 2002US-0404821P.

PR

23-AUG-2002; 2002US-0405368P.

PR

23-AUG-2002; 2002US-0405402P.

PR

23-AUG-2002; 2002US-0405496P.

PR

23-AUG-2002; 2002US-0405631P.

PR

26-AUG-2002; 2002US-0406125P.

PR

04-NOV-2002; 2002US-00287226.

XX

(CURA-) CURAGEN CORP.

Agge ML, Alsebrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS;

Chaudhuri A, Dipippo VA, Edinger SR, Elsen A, Ellerman K;

Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV;

Li L, Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I;

Ooi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK;

Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ;

Vernet CAM, Zerhusen BD, Zhong M;

WPI; 2003-441551/41.

N-PSDB; ADJ94913.

XX

XX New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX

XX Claim 1; SEQ ID NO 142; 800pp; English.

XX

XX The invention relates to novel isolated polypeptides, mature forms of

CC these, or a sequence that is at least 95 % identical to, or having one or

CC more conservative amino acid substitutions in the polypeptides. The

CC polypeptides, nucleic acid molecules and antibodies are useful in the

CC manufacture of a medicament for treating a syndrome associated with a

CC human disease, preferably a NOVX-associated disorder. The nucleic acid

CC molecules, polypeptides and antibodies are useful for treating

CC preventing or diagnosing diseases such as metabolic disorders, diabetes, and

CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and

CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,

CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease,

CC Parkinson's disease, epilepsy, immune disorders (osteoarthritis),

CC hematopoietic disorders, inflammatory skin disorders, asthma, and various

CC dyslipidemias. The nucleic acids and polypeptides may also be used as
 CC targets for the identification of small molecules that modulate or
 CC inhibit e.g. neurogenesis, cell differentiation, cell proliferation,
 CC hematopoiesis, wound healing and angiogenesis, in gene therapy, in
 CC generation of antibodies that bind immunospecifically to NOVX substances
 CC for use in therapeutic or diagnostic methods. The nucleic acids are
 CC further used as hybridization probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. This sequence
 CC corresponds to one of the NOVX polypeptides of the invention.
 XX
 SQ Sequence 1401 AA;

Query Match 65.8%; Score 52; DB 7; Length 1401;
 Best Local Similarity 66.7%; Pred. No. 5.4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
 DB 193 RHTGTTQMEHSSRS 207
 ||| |||: |||

RESULT 27
 ABB61012
 ID ABB61012 standard; protein; 1931 AA.
 AC ABB61012;
 XX
 XX 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 9828.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-0191637P.
 PR
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL05115.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX Disclosure; SEQ ID NO 9828; 2lpp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1931 AA;

Query Match 65.8%; Score 52; DB 4; Length 1931;
 Best Local Similarity 73.3%; Pred. No. 7.7;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
 DB 183 RVVGETNNRSSRS 197
 ||| |||: |||

RESULT 28
 AAG31118
 ID AAG31118 standard; protein; 726 AA.
 AC AAG31118;
 XX
 XX 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 37317.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-00301439.
 XX
 XX 25-FEB-1999; 99US-0121825P.
 PR
 PR 05-MAR-1999; 99US-0123180P.
 PR
 PR 09-MAR-1999; 99US-0123548P.
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us-09-993-399-1.rag

Mon Apr 24 09:14:16 2006

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PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 64.6%; Score 51; DB 3; Length 834;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGTQWQSSRS 15
| | | | | : | | | | |
Db 214 RKIGETSLNRSRS 228

RESULT 31
ABB65183
ID ABB65183 standard; protein; 677 AA.
XX
AC ABB65183;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 22341.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
XX
OS Drosophila melanogaster.

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us-09-993-399-1.rag

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XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL09286.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 22341; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at fcp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 677 AA;
XX
XX Query Match 63.3%; Score 50; DB 4; Length 677;
XX Best Local Similarity 73.3%; Pred. No. 5.6;
XX Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 RHYGETKMNQSSRS 15
XX | | | | | | | | | |
XX Db 213 RAVGATKMNQSSRS 227
XX
XX RESULT 32
XX AAG14279
XX ID AAG14279 standard; protein; 172 AA.
XX
XX AC AAG14279;
XX
XX DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 14079.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; Genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX

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PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR 23-JUN-1999; 99US-0140353P.
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PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.

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PR 19-JUL-1999; 99US-0144331P.
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 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
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 PR 23-JUL-1999; 99US-0145118P.
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 PR 23-JUL-1999; 99US-0145224P.
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 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147493P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
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 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149428P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
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 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157533P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.

PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 62.0%; Score 49; DB 3; Length 172;

Best Local Similarity 72.7%; Pred. No. 1.9;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKMNQR 11

Db 68 RHYNETRINQR 78

RESULT 33

ADC23342

ID ADC23342 standard; protein; 346 AA.

XX AC ADC23342;

XX DT 18-DEC-2003 (first entry)

XX DE Human kinesin-like DNA binding protein (KID) (SeqID 6).

XX KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
 KW cytoskeletal; cardiant; immunomodulator; antiinflammatory; gene therapy;
 KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
 KW cardiac hypertrophy; immune disorder; inflammation.

XX OS Homo sapiens.

XX PN US6387644-B1.

XX PD 14-MAY-2002.

XX PF 28-NOV-2000; 2000US-00724224.

XX PR 20-APR-1999; 99US-00395612.

XX PR 20-JUN-2000; 2000US-00597292.

XX PA (CYTO-) CYTOKINETICS INC.

XX PI Beraud C;

XX DR WPI; 2003-706919/67.

XX DR N-PSDB; ADC23341.

XX PT Identifying a candidate agent as modulator of function of a target
 protein for treating cellular proliferation disorders by adding a

CC for modulators of a motor protein which has microtubule stimulated ATPase
 CC activity, a method of testing for ATPase activity of microtubule motor
 CC proteins, methods to identify candidate agents that bind to a target
 CC protein or act as a modulator of the binding characteristics or
 CC biological activity of a target protein, modulators of the target
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation, for treating disorders associated with kinesin-like DNA
 CC binding protein (KID) and for inhibiting KID. The sequences are useful for
 CC screening for modulators of motor proteins useful for treating cellular
 CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
 CC hypertrophy, immune disorders and inflammation, for treating disorders
 CC associated with KID and for inhibiting KID and for treating autoimmune
 CC diseases, arthritis, graft rejection, inflammatory bowel disease and
 CC proliferation induced after medical procedures including surgery and
 CC angioplasty. This sequence represents a human microtubule motor protein
 CC of the invention.
 XX
 SQ Sequence 346 AA;
 Query Match 62.0%; Score 49; DB 8; Length 346;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RHYGETKMQRSRS 15
 Db 208 RTVGATRLNQRSRS 222
 RESULT 35
 ADQ88357
 ID ADQ88357 standard; protein; 346 AA.
 XX
 AC ADQ88357;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human microtubule motor protein KID #3.
 XX
 KW Human; microtubule motor protein; cellular proliferative disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW wound; inflammation; autoimmune disease; arthritis;
 KW inflammatory bowel disease; solid tumour; skin carcinoma;
 KW breast carcinoma; cervical carcinoma; testicular carcinoma;
 KW bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; bone tumour;
 KW osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.
 XX
 OS Homo sapiens.
 XX
 PN US2004142397-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 09-MAR-2004; 2004US-00797893.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 PR 06-MAR-2002; 2002US-00093317.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI; 2004-552562/53.
 DR N-PSDB; ADQ88356.
 XX
 PT Novel isolated microtubule motor protein, useful for identifying
 PT candidate agent modulating function of protein, for treating cellular
 PT proliferative diseases such as cancer, restenosis, cardiac hypertrophy
 PT and inflammation.
 XX
 PS Claim 5; SEQ ID NO 6; 27pp; English.

PT candidate agent to a mixture of the target protein that
 PT directly/indirectly produces ADP or phosphate.
 XX
 PS Claim 1; SEQ ID NO 6; 26pp; English.
 XX
 CC This invention relates to a novel method for high throughput screening
 CC systems used to identify compounds for the treatment of cellular
 CC proliferation disorders. Specifically, it refers to candidate agents that
 CC are capable of modulating the activity of target proteins having motor
 CC domains, such that the target protein directly or indirectly produces ADP
 CC or phosphate. Furthermore, this activity can be determined using
 CC fluorescence or absorbance readouts. The present invention describes a
 CC method that identifies modulators of the target protein, which is a
 CC kinesin-like DNA binding protein (known as KID) as cytosolic, cardants,
 CC immunomodulators and antiinflammatories. Accordingly, through gene
 CC therapy, they can be used for the treatment of cancer, hyperplasias,
 CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
 CC polypeptide sequence is human KID protein (SeqID 6) of the invention.
 XX
 SQ Sequence 346 AA;
 Query Match 62.0%; Score 49; DB 7; Length 346;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 RHYGETKMQRSRS 15
 Db 208 RTVGATRLNQRSRS 222
 RESULT 34
 ADQ60232
 ID ADQ60232 standard; protein; 346 AA.
 XX
 AC ADQ60232;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human microtubule motor protein #3.
 XX
 KW Human; microtubule motor protein; cellular proliferation disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;
 KW arthritis; graft rejection; inflammatory bowel disease; angioplasty.
 XX
 OS Homo sapiens.
 XX
 PN US6762043-B1.
 XX
 PD 13-JUL-2004.
 XX
 PF 06-MAR-2002; 2002US-00093317.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI; 2004-532491/51.
 DR N-PSDB; ADQ60231.
 XX
 PT New isolated microtubule motor protein, useful for screening modulators
 PT for treating cellular proliferation disorders such as cancer,
 PT hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
 PT inflammation.
 XX
 PS Claim 1; SEQ ID NO 6; 26pp; English.
 XX
 CC The invention relates to human microtubule motor proteins and the nucleic
 CC acids encoding them. The invention also relates to a method of screening

XX The invention relates to microtubule motor proteins and nucleic acid
 CC molecules encoding such proteins. Microtubule motor proteins are useful
 CC for identifying candidate agents modulating the function of protein which
 CC in turn are useful for treating cellular proliferative disorders such as
 CC cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders,
 CC wounds and inflammation. Other disorders treated include autoimmune
 CC disease, arthritis, inflammatory bowel disease, solid tumours such as
 CC skin carcinomas, breast carcinomas, cervical carcinomas, testicular
 CC carcinomas, bronchogenic carcinoma, alveolar carcinoma, adenocarcinoma,
 CC tumour of bone such as osteogenic sarcoma, multiple myeloma, malignant
 CC melanoma etc. The present sequence is a human microtubule motor protein
 CC KID polypeptide.

XX Sequence 346 AA;
 SQ

Query Match 62.0%; Score 49; DB 8; Length 346;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
 | | | | | | | | | |
 Db 208 RTVGATRLNQSRSS 222

RESULT 36
 ADC23338
 ID ADC23338 standard; protein; 370 AA.
 XX
 AC ADC23338;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human kinesin-like DNA binding protein (KID) (SeqID 2).
 XX
 KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
 KW cytosolic; cardiac; immunomodulator; antiinflammatory; gene therapy;
 KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
 KW cardiac hypertrophy; immune disorder; inflammation.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Encoded by ATGCA"
 XX
 XX US6387644-B1.
 XX
 XX 14-MAY-2002.
 XX
 XX 28-NOV-2000; 2000US-00724224.
 XX
 XX 20-APR-1999; 99US-00295612.
 XX
 XX 20-JUN-2000; 2000US-00597292.
 XX
 XX (CYTO-) CYTOKINETICS INC.
 XX
 XX Beraud C;
 XX
 XX WPI; 2003-706919/67.
 XX
 XX N-PSDB; ADC23337.
 XX
 XX Identifying a candidate agent as modulator of function of a target
 XX protein for treating cellular proliferation disorders by adding a
 XX candidate agent to a mixture of the target protein that
 XX directly/indirectly produces ADP or phosphate.
 XX
 XX Claim 1; SEQ ID NO 2; 26pp; English.
 XX
 XX This invention relates to a novel method for high throughput screening
 XX systems used to identify compounds for the treatment of cellular
 XX proliferation disorders. Specifically, it refers to candidate agents that
 XX are capable of modulating the activity of target proteins having motor

CC domains, such that the target protein directly or indirectly produces ADP
 CC or phosphate. Furthermore, this activity can be determined using
 CC fluorescence or absorbance readouts. The present invention describes a
 CC method that identifies modulators of the target protein, which is a
 CC kinesin-like DNA binding protein (known as KID) as cytosolic, cardiac,
 CC immunomodulators and antiinflammatory. Accordingly, through gene
 CC therapy, they can be used for the treatment of cancer, hyperplasias,
 CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
 CC polypeptide sequence is human KID protein (SeqID 2) of the invention.

XX Sequence 370 AA;
 SQ

Query Match 62.0%; Score 49; DB 7; Length 370;
 Best Local Similarity 66.7%; Pred. No. 4.3;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
 | | | | | | | | | |
 Db 232 RTVGATRLNQSRSS 246

RESULT 37
 ADQ60228
 ID ADQ60228 standard; protein; 370 AA.
 XX
 AC ADQ60228;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human microtubule motor protein #1.
 XX
 KW Human; microtubule motor protein; cellular proliferation disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;
 KW arthritis; graft rejection; inflammatory bowel disease; angioplasty.
 XX
 OS Homo sapiens.
 XX
 XX US6762043-B1.
 XX
 XX 13-JUL-2004.
 XX
 XX 06-MAR-2002; 2002US-00093317.
 XX
 XX 20-APR-1999; 99US-00295612.
 XX
 XX 20-JUN-2000; 2000US-00597292.
 XX
 XX 28-NOV-2000; 2000US-00724224.
 XX
 XX (CYTO-) CYTOKINETICS INC.
 XX
 XX Beraud C;
 XX
 XX WPI; 2004-532491/51.
 XX
 XX New isolated microtubule motor protein, useful for screening modulators
 XX for treating cellular proliferation disorders such as cancer,
 XX hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
 XX inflammation.
 XX
 XX Claim 1; SEQ ID NO 2; 26pp; English.
 XX
 XX The invention relates to human microtubule motor proteins and the nucleic
 XX acids encoding them. The invention also relates to a method of screening
 XX for modulators of a motor protein which has microtubule stimulated ATPase
 XX activity, a method of testing for ATPase activity of microtubule motor
 XX proteins, methods to identify candidate agents that bind to a target
 XX protein or act as a modulator of the binding characteristics or
 XX biological activity of a target protein, modulators of the target
 XX protein, and methods of treating cellular proliferation disorders such as
 XX cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 XX and inflammation, for treating disorders associated with kinesin-like DNA
 XX binding protein (KID) and for inhibiting KID. The sequences are used for
 XX screening for modulators of motor proteins useful for treating cellular

CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
CC hypertrophy, immune disorders and inflammation, for treating disorders
CC associated with KID and for inhibiting KID and for treating autoimmune
CC diseases, arthritis, graft rejection, inflammatory bowel disease and
CC proliferation induced after medical procedures including surgery and
CC angioplasty. This sequence represents a human microtubule motor protein
CC of the invention. Note: The specification states that this sequence is
CC encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
CC appear to be the case.
XX
XX
SQ Sequence 370 AA;
Query Match 62.0%; Score 49; DB 8; Length 370;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMNQRSSRS 15
DB 232 RTVGATRLNQRSSRS 246
RESULT 39
AAB56650
ID AAB56650 standard; protein; 460 AA.
XX
XX AAB56650;
XX
XX
DT 13-MAR-2001 (first entry)
DE Human prostate cancer antigen protein sequence SEQ ID NO:1228.
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
XX neuroprotective; cytostatic; cardioprotective; immunomodulatory; muscular;
XX vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
XX antibacterial; gene therapy; neural; immune; reproductive; renal;
XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
XX wound; infectious disease.
XX Homo sapiens.
XX
XX WO200055174-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005988.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
XX N-PSDB; AAF15853.
XX
XX Prostate cancer associated gene sequences, referred to as prostate cancer
XX antigens, useful for treatment, prevention, and diagnosis of disorders
XX such as prostate cancer.
XX
XX Claim 11; Page 1649-1651; 2338pp; English.
XX
XX AAF15566 to AAF16505 encode the human prostate cancer associated
XX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
XX The prostate cancer antigens can have neuroprotective, cytostatic,
XX cardioprotective, immunomodulatory, muscular, vulnary, gastrointestinal,
XX proliferative diseases such as cancer, restenosis, cardiac hypertrophy
XX and inflammation.
XX
XX Claim 5; SEQ ID NO 2; 27pp; English.
XX
XX The invention relates to microtubule motor proteins and nucleic acid
XX molecules encoding such proteins. Microtubule motor proteins are useful
XX for identifying candidate agents modulating the function of protein which

CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
CC hypertrophy, immune disorders and inflammation, for treating disorders
CC associated with KID and for inhibiting KID and for treating autoimmune
CC diseases, arthritis, graft rejection, inflammatory bowel disease and
CC proliferation induced after medical procedures including surgery and
CC angioplasty. This sequence represents a human microtubule motor protein
CC of the invention. Note: The specification states that this sequence is
CC encoded by the nucleic acid featured as SEQ ID NO:1, but this does not
CC appear to be the case.
XX
XX
SQ Sequence 370 AA;
Query Match 62.0%; Score 49; DB 8; Length 370;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMNQRSSRS 15
DB 232 RTVGATRLNQRSSRS 246
RESULT 38
ADQ88353
ID ADQ88353 standard; protein; 370 AA.
XX
XX ADQ88353;
XX
XX
DT 07-OCT-2004 (first entry)
DE Human microtubule motor protein KID #1.
XX Human; microtubule motor protein; cellular proliferative disorder;
XX cancer; hyperplasias; restenosis; cardiac hypertrophy; immune disorder;
XX wound; inflammation; autoimmune disease; arthritis;
XX inflammatory bowel disease; solid tumour; skin carcinoma;
XX breast carcinoma; cervical carcinoma; testicular carcinoma;
XX bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; bone tumour;
XX osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /note= "Encoded by ATGCA"
XX
XX US2004142397-A1.
XX
XX 22-JUL-2004.
XX
XX 09-MAR-2004; 2004US-00797893.
XX
XX 20-APR-1999; 99US-00295612.
XX 20-JUN-2000; 2000US-00597292.
XX 28-NOV-2000; 2000US-00724224.
XX 06-MAR-2002; 2002US-00093317.
XX
XX (CYTO-) CYTOKINETICS INC.
XX
XX Beraud C;
XX
XX WPI; 2004-552562/53.
XX N-PSDB; ADQ88352.
XX
XX Novel isolated microtubule motor protein, useful for identifying
XX candidate agent modulating function of protein, for treating cellular
XX proliferative diseases such as cancer, restenosis, cardiac hypertrophy
XX and inflammation.
XX
XX Claim 5; SEQ ID NO 2; 27pp; English.
XX
XX The invention relates to microtubule motor proteins and nucleic acid
XX molecules encoding such proteins. Microtubule motor proteins are useful
XX for identifying candidate agents modulating the function of protein which

CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 460 AA;

Query Match 62.0%; Score 49; DB 3; Length 460;
 Best Local Similarity 66.7%; Pred. No. 5.5;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 | | | | |
 DB 210 RTVGATRLNQSRSS 224

RESULT 40
 ADC23344
 ID ADC23344 standard; protein; 487 AA.
 AC ADC23344;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human kinesin-like DNA binding protein (KID) (SeqID 8).
 XX
 KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
 KW cytoskeletal; cardiant; immunomodulator; antiinflammatory; gene therapy;
 KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
 KW cardiac hypertrophy; immune disorder; inflammation.
 XX
 OS Homo sapiens.
 XX
 XX US6387644-B1.
 PN
 PD 14-MAY-2002.
 XX
 XX 28-NOV-2000; 2000US-00724224.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 PI Beraud C;
 XX
 DR WPI; 2003-706919/67.
 DR N-PSDB; ADC23343.

Identifying a candidate agent as modulator of function of a target
 protein for treating cellular proliferation disorders by adding a
 candidate agent to a mixture of the target protein that
 directly/indirectly produces ADP or phosphate.
 Claim 1; SEQ ID NO 8; 26pp; English.
 This invention relates to a novel method for high throughput screening
 systems used to identify compounds for the treatment of cellular
 proliferation disorders. Specifically, it refers to candidate agents that
 are capable of modulating the activity of target proteins having motor
 domains, such that the target protein directly or indirectly produces ADP
 or phosphate. Furthermore, this activity can be determined using
 fluorescence or absorbance readouts. The present invention describes a
 method that identifies modulators of the target protein, which is a
 kinesin-like DNA binding protein (known as KID) as cytostatic, cardiants,
 immunomodulators and antiinflammatories. Accordingly, through gene
 therapy, they can be used for the treatment of cancer, hyperplasias,
 restenosis, cardiac hypertrophy, immune disorders and inflammation. This
 polypeptide sequence is human KID protein (SeqID 8) of the invention.

Query Match 62.0%; Score 49; DB 7; Length 487;
 Best Local Similarity 66.7%; Pred. No. 5.9;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSRSS 15
 | | | | |
 DB 208 RTVGATRLNQSRSS 222

RESULT 41
 ADQ60234
 ID ADQ60234 standard; protein; 487 AA.

AC ADQ60234;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human microtubule motor protein #4.

XX
 KW Human; microtubule motor protein; cellular proliferation disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;
 KW arthritis; graft rejection; inflammatory bowel disease; angioplasty.
 XX
 OS Homo sapiens.
 XX
 XX US6762043-B1.
 PN
 PD 13-JUL-2004.
 XX
 PF 06-MAR-2002; 2002US-00093317.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 XX
 PA (CYTO-) CYTOKINETICS INC.

XX Beraud C;
 XX
 DR WPI; 2004-532491/51.
 DR N-PSDB; ADQ60233.
 XX
 PT New isolated microtubule motor protein, useful for screening modulators
 PT for treating cellular proliferation disorders such as cancer,
 PT hyperplasias, restenosis, cardiac hypertrophy, immune disorders and
 PT inflammation.
 XX
 PS Claim 1; SEQ ID NO 8; 26pp; English.
 XX
 CC The invention relates to human microtubule motor proteins and the nucleic
 CC acids encoding them. The invention also relates to a method of screening
 CC for modulators of a motor protein which has microtubule stimulated ATPase
 CC activity, a method of testing for ATPase activity of microtubule motor
 CC proteins, methods to identify candidate agents that bind to a target
 CC protein or act as a modulator of the binding characteristics or
 CC biological activity of a target protein, modulators of the target
 CC protein, and methods of treating cellular proliferation disorders such as
 CC cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders
 CC and inflammation, for treating disorders associated with kinesin-like DNA
 CC binding protein (KID) and for inhibiting KID. The sequences are used for
 CC screening for modulators of motor proteins useful for treating cellular
 CC proliferation disorders such as cancer, hyperplasias, restenosis, cardiac
 CC hypertrophy, immune disorders and inflammation, for treating disorders
 CC associated with KID and for inhibiting KID and for treating autoimmune
 CC diseases, arthritis, graft rejection, inflammatory bowel disease and
 CC proliferation induced after medical procedures including surgery and
 CC angioplasty. This sequence represents a human microtubule motor protein
 CC of the invention.

XX Sequence 487 AA;

Query Match 62.0%; Score 49; DB 8; Length 487;
 Best Local Similarity 66.7%; Pred. No. 5.9;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
 DB 208 RTVGATRLNQSSRS 222

RESULT 42
 ADQ88359
 ID ADQ88359 standard; protein; 487 AA.
 XX
 AC ADQ88359;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human microtubule motor protein KID #4.
 XX
 KW Human; microtubule motor protein; cellular proliferative disorder;
 KW cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;
 KW wound; inflammation; autoimmune disease; arthritis;
 KW inflammatory bowel disease; solid tumour; skin carcinoma;
 KW breast carcinoma; cervical carcinoma; testicular carcinoma;
 KW bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; bone tumour;
 KW osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.
 XX
 OS Homo sapiens.
 XX
 PN US2004142397-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 09-MAR-2004; 2004US-00797893.
 XX
 PR 20-APR-1999; 99US-00295612.
 PR 20-JUN-2000; 2000US-00597292.
 PR 28-NOV-2000; 2000US-00724224.
 PR 06-MAR-2002; 2002US-00093317.
 XX
 PA (CYTO-) CYTOKINETICS INC.
 XX
 PI Beraud C;
 XX
 DR WPI; 2004-552562/53.
 DR N-PSDB; ADQ88359.
 XX
 PT Novel isolated microtubule motor protein, useful for identifying
 PT candidate agent modulating function of protein, for treating cellular
 PT proliferative diseases such as cancer, restenosis, cardiac hypertrophy
 PT and inflammation.
 XX
 PS Claim 5; SEQ ID NO 8; 27pp; English.
 XX
 CC The invention relates to microtubule motor proteins and nucleic acid
 CC molecules encoding such proteins. Microtubule motor proteins are useful
 CC for identifying candidate agents modulating the function of protein which
 CC in turn are useful for treating cellular proliferative disorders such as
 CC cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders,
 CC wounds and inflammation. Other disorders treated include autoimmune
 CC disease, arthritis, inflammatory bowel disease, solid tumours such as
 CC skin carcinomas, breast carcinomas, cervical carcinomas, testicular
 CC carcinomas, bronchogenic carcinoma, alveolar carcinoma, adenocarcinoma,
 CC tumour of bone such as osteogenic sarcoma, multiple myeloma, malignant
 CC melanoma etc. The present sequence is a human microtubule motor protein
 CC KID polypeptide.
 XX
 SQ Sequence 487 AA;
 Query Match 62.0%; Score 49; DB 8; Length 487;
 Best Local Similarity 66.7%; Pred. No. 5.9;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
 DB 208 RTVGATRLNQSSRS 222

RESULT 43
 ADK40973
 ID ADK40973 standard; protein; 490 AA.
 XX
 AC ADK40973;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Novel human kinase protein #80.
 XX
 KW cytosolic; immunomodulator; cardiant; neuroprotective; nootropic;
 KW antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;
 KW analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;
 KW cancer; peripheral nervous system; central nervous system;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
 KW amyotrophic lateral sclerosis; viral infection; prion infection;
 KW ocular disease; migraine; pain; sexual dysfunction; mood disorder;
 KW attention disorder; cognition disorder; hypotension; hypertension;
 KW psychotic disorder; neurological disorder; dyskinesia;
 KW metabolic disorder; organ transplant rejection; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057841-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 31-DEC-2002; 2002WO-US041687.
 XX
 PR 31-DEC-2001; 2001US-0343169P.
 XX
 PA (GRIG/) GRIGORIEV I V.
 PA (SUDA/) SUDARSANAM S.
 XX
 PI Grigoriev IV, Sudarsanam S;
 XX
 DR WPI; 2003-587115/55.
 XX
 PT New isolated, enriched or purified nucleic acid molecule encoding a
 PT kinase polypeptide, useful for treating cancer, immune-related diseases,
 PT cardiovascular disease, brain or neuronal-associated diseases and
 PT metabolic disorders.
 XX
 PS Claim 1; SEQ ID NO 80; 491pp; English.
 XX
 CC The invention relates to novel isolated, enriched or purified nucleic acid
 CC molecules encoding a kinase polypeptide. The nucleic acid molecule
 CC comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a
 CC complement of (a); (c) hybridizes under stringent conditions to (a) and
 CC encodes a naturally occurring kinase polypeptide; (d) encodes the
 CC polypeptide in (a), except that it lacks one or more, but not all, of an
 CC N-terminal domain, C-terminal catalytic domain, a spacer region and a C-
 CC terminal domain, a coiled-coil structure region, a catalytic domain, a C-
 CC terminal tail; or (e) is a complement of (d). The nucleic acid molecules,
 CC polypeptides, methods and substance are useful for treating cancers,
 CC immune-related diseases or disorders, cardiovascular disease, brain or
 CC neuronal-associated diseases, and metabolic disorders. The disorders are
 CC preferably cancers of the tissues or of hematopoietic origin, diseases of
 CC the central or peripheral nervous system, Alzheimer's disease,
 CC Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,
 CC viral infections, infections caused by prions, infections caused by
 CC bacteria, infections caused by fungi, ocular diseases, migraines, pain,
 CC sexual dysfunction, mood disorders, attention disorders, cognition
 CC disorders, hypotension, hypertension, psychotic disorders, neurological
 CC disorders, dyskinesias, metabolic disorders and organ transplant
 CC rejection. This sequence corresponds to one of the kinase polypeptides of
 CC the invention.
 XX
 SQ Sequence 490 AA;
 Query Match 62.0%; Score 49; DB 7; Length 490;

Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
| | | | | | | | | |
Db 240 RTVGATRLNQSRSS 254

RESULT 44
ADRI5692
ID ADR15692 standard; protein; 490 AA.
XX
AC ADR15692;
XX
DT 04-NOV-2004 (first entry)
XX
DE Kinase 730440 hCT1809245, SEQ ID 85.
XX
KW Cytostatic; Cardiovascular; Neuroprotective; Nootropic; Antiparkinsonian;
KW Virucide; Cerebroprotective; Antibacterial; Fungicide; Ophthalmological;
KW Antimigraine; Analgesic; Endocrine; Tranquillizer; Hypotensive;
KW Immunosuppressive; Gene Therapy; Kinase; enzyme; cancer;
KW Immune-related disease; cardiovascular disease;
KW neuronal-associated disease; metabolic disorder.
XX
OS Homo sapiens.
XX
PN WO2004069154-A2.
XX
PD 19-AUG-2004.
XX
PF 28-JAN-2003; 2003WO-US002234.
XX
PR 28-JAN-2003; 2003WO-US002234.
XX
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
XX
PI Grigoriev IV, Sudarsanam S;
XX
DR WPI; 2004-604329/58.
DR N-PSDB; ADRI5709.
XX
XX New isolated, enriched, or purified kinase nucleic acids and
PT polypeptides, useful for diagnosing or treating kinase-related diseases
PT and conditions, e.g. cardiovascular disease, brain or neuronal-associated
PT diseases, or metabolic disorders.
XX
PS Claim 7; Fig 2; 496pp; English.
XX
CC The present invention relates to a method for detecting remote
CC polypeptide homologues, comprising analysis of conserved secondary
CC structure pattern in a protein family, and conserved active site amino
CC acid residues. The analyses are used to identify conserved residues
CC embedded into the secondary structure pattern (CRISP), which are used to
CC detect remote homologues of the referent protein family, wherein said
CC referent protein family is the protein kinase family. The present
CC sequence is a kinase, used to illustrate the method of the invention. The
CC kinases are useful for diagnosing or treating various kinase-related
CC diseases and conditions. Diseases or disorders include cancers, immune-
CC related diseases and disorders, cardiovascular disease, brain or neuronal
CC -associated diseases, or metabolic disorders. Preferably, the diseases or
CC disorders are cancers of tissues, cancers of haematopoietic origin,
CC diseases of the central nervous system, diseases of the peripheral
CC nervous system, Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, viral infections, infections
CC caused by prions, infections caused by bacteria, viral infections, infections
CC fungi, or ocular diseases. The disease or disorder is also migraines,
CC pain, sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypertension, psychotic disorders, neurological disorders,
CC dyskinesias, metabolic disorders, or organ transplant rejection.
XX
SQ Sequence 490 AA;

Query Match 62.0%; Score 49; DB 8; Length 490;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
| | | | | | | | | |
Db 240 RTVGATRLNQSRSS 254

RESULT 45
ADC23340
ID ADC23340 standard; protein; 512 AA.
XX
AC ADC23340;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human kinesin-like DNA binding protein (KID) (SeqID 4).
XX
KW human; enzyme; motor domain; kinesin-like DNA binding protein; KID;
KW cytoskeletal; cardiant; immunomodulator; antiinflammatory; gene therapy;
KW cancer; hyperplasia; restenosis; cellular proliferation disorder;
KW cardiac hypertrophy; immune disorder; inflammation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "Encoded by CA"
XX
PN US6387644-B1.
XX
PD 14-MAY-2002.
XX
PF 28-NOV-2000; 2000US-00724224.
XX
PR 20-APR-1999; 99US-00295612.
PR 20-JUN-2000; 2000US-00597292.
XX
PA (CYTO-) CYTOKINETICS INC.
XX
PI Beraud C;
XX
DR WPI; 2003-706919/67.
DR N-PSDB; ADC23339.
XX
PT Identifying a candidate agent as modulator of function of a target
PT protein for treating cellular proliferation disorders by adding a
PT candidate agent to a mixture of the target protein that
PT directly/indirectly produces ADP or phosphate.
XX
PS Claim 1; SEQ ID NO 4; 26pp; English.
XX
CC This invention relates to a novel method for high throughput screening
CC systems used to identify compounds for the treatment of cellular
CC proliferation disorders. Specifically, it refers to candidate agents that
CC are capable of modulating the activity of target proteins having motor
CC domains, such that the target protein directly or indirectly produces ADP
CC or phosphate. Furthermore, this activity can be determined using
CC fluorescence or absorbance readouts. The present invention describes a
CC method that identifies modulators of the target protein, which is a
CC kinesin-like DNA binding protein (known as KID) as cytoskeletal, cardiants,
CC immunomodulators and antiinflammatory. Accordingly, through gene
CC therapy, they can be used for the treatment of cancer, hyperplasias,
CC restenosis, cardiac hypertrophy, immune disorders and inflammation. This
CC polypeptide sequence is human KID protein (SeqID 4) of the invention.
XX
SQ Sequence 512 AA;

Query Match 62.0%; Score 49; DB 7; Length 512;
Best Local Similarity 66.7%; Pred. No. 6.2;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY	1	RHYGETKNQRRSSRS	15
Db	233	RTVGATRLNQRSSRS	247
RESULT 46			
ID	ADQ60230	standard; protein; 512 AA.	
AC	ADQ60230;		
DT	23-SEP-2004	(first entry)	
DE	Human microtubule motor protein #2.		
KW	Human; microtubule motor protein; cellular proliferation disorder;		
KW	cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;		
KW	inflammation; kinesin-like DNA binding protein; KID; autoimmune disease;		
KW	arthritis; graft rejection; inflammatory bowel disease; angioplasty.		
OS	Homo sapiens.		
PN	US6762043-B1.		
PD	13-JUL-2004.		
PF	06-MAR-2002; 2002US-00093317.		
PR	20-APR-1999; 99US-00295612.		
PR	20-JUN-2000; 2000US-00597292.		
PR	28-NOV-2000; 2000US-00724224.		
XX	(CYTO-) CYTOKINETICS INC.		
PI	Beraud C;		
DR	WPI; 2004-532491/51.		
XX	New isolated microtubule motor protein, useful for screening modulators		
PT	for treating cellular proliferation disorders such as cancer,		
PT	hyperplasias, restenosis, cardiac hypertrophy, immune disorders and		
PT	inflammation.		
XX	Claim 1; SEQ ID NO 4; 26pp; English.		
XX	The invention relates to human microtubule motor proteins and the nucleic		
CC	acids encoding them. The invention also relates to a method of screening		
CC	for modulators of a motor protein which has microtubule stimulated Arpase		
CC	activity, a method of testing for Arpase activity of microtubule motor		
CC	proteins, methods to identify candidate agents that bind to a target		
CC	protein or act as a modulator of the binding characteristics or		
CC	biological activity of a target protein, modulators of the target		
CC	protein, and methods of treating cellular proliferation disorders such as		
CC	cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders		
CC	and inflammation, for treating disorders associated with kinesin-like DNA		
CC	binding protein (KID) and for inhibiting KID. The sequences are used for		
CC	screening for modulators of motor proteins useful for treating cellular		
CC	proliferation disorders such as cancer, hyperplasias, restenosis, cardiac		
CC	hypertrophy, immune disorders and inflammation, for treating autoimmune		
CC	diseases, arthritis, graft rejection, inflammatory bowel disease and		
CC	proliferation induced after medical procedures including surgery and		
CC	angioplasty. This sequence represents a human microtubule motor protein		
CC	of the invention. Note: The specification states that this sequence is		
CC	encoded by the nucleic acid featured as SEQ ID NO:3, but this does not		
CC	appear to be the case.		
SQ	Sequence 512 AA;	Query Match	62.0%; Score 49; DB 8; Length 512;
		Best Local Similarity	66.7%; Pred. No. 6.2;
		Matches	10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY	1	RHYGETKNQRRSSRS	15
Db	233	RTVGATRLNQRSSRS	247
RESULT 47			
ID	ADQ88355	standard; protein; 512 AA.	
AC	ADQ88355;		
DT	07-OCT-2004	(first entry)	
DE	Human microtubule motor protein KID #2.		
KW	Human; microtubule motor protein; cellular proliferative disorder;		
KW	cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder;		
KW	wound; inflammation; autoimmune disease; arthritis;		
KW	inflammatory bowel disease; solid tumour; skin carcinoma;		
KW	breast carcinoma; cervical carcinoma; testicular carcinoma;		
KW	bronchogenic carcinoma; alveolar carcinoma; adenocarcinoma; bone tumour;		
KW	osteogenic sarcoma; multiple myeloma; malignant melanoma; KID.		
OS	Homo sapiens.		
PN			
PD			
PF			
PR			
PR			
PR			
PR			
XX	(CYTO-) CYTOKINETICS INC.		
PI	Beraud C;		
DR	WPI; 2004-552562/53.		
DR	N-PSDB; ADQ88354.		
XX	Novel isolated microtubule motor protein, useful for identifying		
PT	candidate agent modulating function of protein, for treating cellular		
PT	proliferative diseases such as cancer, restenosis, cardiac hypertrophy		
PT	and inflammation.		
XX	Claim 5; SEQ ID NO 4; 27pp; English.		
XX	The invention relates to microtubule motor proteins and nucleic acid		
CC	molecules encoding such proteins. Microtubule motor proteins are useful		
CC	for identifying candidate agents modulating the function of protein which		
CC	in turn are useful for treating cellular proliferative disorders such as		
CC	cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders,		
CC	wounds and inflammation. Other disorders treated include autoimmune		
CC	disease, arthritis, inflammatory bowel disease, solid tumours such as		
CC	skin carcinomas, breast carcinomas, cervical carcinomas, testicular		
CC	carcinomas, bronchogenic carcinoma, alveolar carcinoma, adenocarcinoma,		
CC	tumour of bone such as osteogenic sarcoma, multiple myeloma, malignant		
CC	melanoma etc. The present sequence is a human microtubule motor protein		
CC	KID polypeptide.		
XX	Sequence 512 AA;	Query Match	62.0%; Score 49; DB 8; Length 512;
		Best Local Similarity	66.7%; Pred. No. 6.2;
		Matches	10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
 DB 233 RTVGATRLNQSSRS 247

RESULT 48
 ADQ09240
 ID ADQ09240 standard; protein; 665 AA.
 XX
 AC ADQ09240;
 DT 23-SEP-2004 (first entry)
 XX
 DE Human KNSL4 protein SEQ ID NO:425.
 XX
 KW thanatos-associated protein; THAP; THAP responsive gene; THAP family;
 KW THAP responsive element; angiogenesis; inflammation; metastasis; cancer;
 KW apoptosis; cardiovascular disease; neurodegenerative disease; chemokine;
 KW antiangiogenic; antiinflammatory; cardiovascular; cytostatic;
 KW neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004055050-A2.
 XX
 PD 01-JUL-2004.
 XX
 XX 10-DEC-2003; 2003WO-IB006434.
 XX
 XX 10-DEC-2002; 2002US-0432699P.
 PR
 PR 03-JUL-2003; 2003US-0485027P.
 XX
 PA (ENDO-) ENDOCUBE SAS.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Girard J, Amalric F, Roussigne M, Clouaire T;
 PI WPI; 2004-525034/50.
 DR N-PSDB; ADQ09241.
 DR
 XX
 PT Modulating expression of a Thanatos (death)-Associated Protein (THAP)
 PT responsive gene for preventing or treating e.g. cancer or inflammation,
 PT comprises modulating the interaction of a THAP polypeptide with a nucleic
 PT acid.
 XX
 PS Example 47; SEQ ID NO 425; 612pp; English.
 XX
 CC The present invention describes a method for modulating the expression of
 CC a thanatos (death)-associated protein (THAP) responsive gene. The method
 CC comprises modulating the interaction of a THAP-family polypeptide or its
 CC biological fragment with a nucleic acid, and so enhancing or repressing
 CC the expression of the THAP responsive gene. Also described: (1) a method
 CC of modulating the expression of a gene responsive to a THAP/chemokine
 CC complex; (2) a pharmaceutical composition comprising a THAP responsive
 CC element in a pharmaceutical carrier; (3) a transcription factor decoy
 CC consisting essentially of a THAP responsive element; (4) a cell
 CC comprising a transcription factor decoy described above; (5) methods of
 CC modulating the interaction between a nucleic acid and a THAP-family
 CC polypeptide or its biological fragment, or a nucleic acid and a
 CC THAP/chemokine complex; (6) a vector packaging cell line comprising a
 CC cell comprising a viral vector which comprises a promoter operably linked
 CC to a nucleic acid encoding a THAP-family polypeptide or its biological
 CC fragment; (7) a method of constructing a cell which expresses a
 CC recombinant THAP-family polypeptide; (8) a method of ameliorating
 CC symptoms associated with a condition mediated by a THAP/chemokine complex
 CC ; (9) methods of identifying a test compound that modulates transcription
 CC at a THAP responsive element or that modulates the transport of a
 CC chemokine into the nucleus; (10) methods for reducing the symptoms
 CC associated with a condition selected from excessive or insufficient
 CC angiogenesis, inflammation, metastasis of a cancerous tissue, excessive
 CC or insufficient apoptosis, cardiovascular disease and neurodegenerative

CC diseases; symptoms associated with a condition resulting from the
 CC activity of a chemokine or a THAP-family polypeptide in an individual; or
 CC symptoms associated with transcriptional repression or activation
 CC mediated by a THAP-family polypeptide in an individual; (11) a vector
 CC comprising a THAP responsive promoter operably linked to a nucleic acid
 CC encoding a detectable product; (12) a genetically engineered cell
 CC comprising the vector described above or that expresses a THAP-family
 CC polypeptide or its biological fragment; (13) an in vitro transcription
 CC reaction comprising a nucleic acid comprising a THAP responsive promoter,
 CC ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-
 CC family polypeptide that does not bind to a chemokine. The pharmaceutical
 CC composition has antiangiogenic, antiinflammatory, cardiovascular,
 CC cytostatic, neuroprotective and osteopathic activities, and can be used
 CC as a THAP and THAP synthesis modulator. The composition can be used for
 CC modulating the expression of a THAP responsive gene. Modulation is useful
 CC for reducing symptoms of conditions such as excessive or insufficient
 CC angiogenesis, inflammation, metastasis of a cancerous tissue, excessive
 CC or insufficient apoptosis, cardiovascular disease or neurodegenerative
 CC diseases. The present sequence is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 665 AA;

Query Match 62.0%; Score 49; DB 8; Length 665;
 Best Local Similarity 66.7%; Pred No. 8.2;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
 DB 233 RTVGATRLNQSSRS 246

RESULT 49

ABM81748
 ID ABM81748 standard; protein; 665 AA.

XX
 AC ABM81748;

XX
 DT 18-NOV-2004 (first entry)

XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO59491, SEQ:4508.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.

XX Homo sapiens.

XX WO2004030615-A2.

PN 15-APR-2004.

PD 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX DR N-PSDB; ACN40003.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 4508; 7273pp; English.

binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of treating cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents a murine cancer-associated protein of the invention.

Sequence 2033 AA;

Query Match 62.0%; Score 49; DB 9; Length 2033;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
DB 1222 RAVGATRLNQSRSS 1236

Search completed: April 21, 2006, 13:38:09
Job time : 224 secs

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

Sequence 665 AA;

Query Match 62.0%; Score 49; DB 8; Length 665;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
DB 232 RTVGATRLNQSRSS 246

RESULT 50

ADZ13122
ID ADZ13122 standard; protein; 2033 AA.

AC ADZ13122;

DT 16-JUN-2005 (first entry)

XX Murine cancer-associated protein #70.

XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm; cytostatic.

OS Mus sp.

XX WO2005031001-A2.

XX 07-APR-2005.

XX 23-SEP-2004; 2004WO-US031617.

XX 23-SEP-2003; 2003US-00669920.

XX (CHIR) CHIRON CORP.

XX Morris DW, Malandro MS;

XX WPI; 2005-273395/28.

XX N-PSDB; ADZ13121.

XX Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probes.

XX Disclosure; SEQ ID NO 642; 198pp; English.

XX The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which

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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:38:26 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGKMNQRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	2663	1 S28261	centromere protein
2	69	87.3	2954	2 T14156	kinesin-related pr
3	58	73.4	823	2 T52425	kinesin-like prote
4	58	73.4	888	2 D94619	protein T30846.9 [
5	54	68.4	955	2 A47334	LcKin kinesin-rela
6	51	64.6	581	2 F84599	probable kinesin h
7	51	64.6	834	2 T06055	hypothetical prote
8	50	63.3	1459	2 T30196	kinesin motor prot
9	49	62.0	198	2 E86183	hypothetical prote
10	49	62.0	665	2 S62328	kinesin-like DNA b
11	48	60.8	1070	2 T06733	kinesin homolog F2
12	47	59.5	670	2 T29898	kinesin protein OS
13	47	59.5	672	2 S54351	kinesin osm-3 - Ca
14	47	59.5	754	2 S48020	kinesin-related pr
15	47	59.5	793	2 S34830	kinesin-related pr
16	46	58.2	102	2 E85814	hypothetical prote
17	46	58.2	108	2 E90966	hypothetical prote
18	46	58.2	127	2 G64960	probable membrane
19	46	58.2	932	2 T49235	kinesin-like prote
20	45	57.0	143	2 C44259	kinesin heavy chai
21	45	57.0	315	2 AF1393	glycosyl transfera
22	45	57.0	315	2 A11768	glycosyl transfera
23	45	57.0	777	2 C85065	kinesin-like prote
24	45	57.0	963	1 A41919	kinesin heavy chai
25	45	57.0	967	1 A31075	kinesin heavy chai
26	45	57.0	975	1 A34097	kinesin heavy chai
27	45	57.0	1027	2 S37711	kinesin heavy chai
28	45	57.0	1031	1 A38713	kinesin heavy chai
29	45	57.0	1032	2 I38510	neuronal kinesin h

30	44	55.7	294	2 S38983	kinesin-related pr
31	44	55.7	706	1 C42640	kinesin-related pr
32	44	55.7	742	1 S58691	kinesin-related pr
33	44	55.7	987	2 B96766	protein kinesin F2
34	44	55.7	1130	2 T21134	hypothetical prote
35	43	54.4	332	2 C48835	kinesin-like prote
36	43	54.4	701	1 B44259	kinesin-related pr
37	43	54.4	747	1 A57107	kinesin-related pr
38	43	54.4	786	2 A53939	kinesin homolog KH
39	43	54.4	968	2 T45746	hypothetical prote
40	43	54.4	1056	2 C96661	kinesin-like prote
41	43	54.4	1263	2 T13465	hypothetical prote
42	42	53.2	699	1 S38982	kinesin-related pr
43	42	53.2	861	2 T00434	probable kinesin h
44	41	51.9	573	2 F26691	probable fumarate
45	41	51.9	770	1 A44337	kinesin-related pr
46	41	51.9	832	2 T38749	kinesin-like prote
47	41	51.9	1265	2 T03792	kinesin-related pr
48	41	51.9	1265	2 T07397	kinesin heavy chai
49	40	50.6	202	2 D85058	hypothetical prote
50	40	50.6	219	2 A75088	hypothetical prote
51	40	50.6	535	2 S56147	GCN20-2 protein -
52	40	50.6	784	1 A55236	kinesin-related pr
53	40	50.6	1075	2 T45570	kinesin-like prote
54	40	50.6	1142	2 S59359	GIN4 protein - yea
55	39.5	50.0	738	2 S32372	transforming prote
56	39	49.4	447	2 S76033	hypothetical prote
57	39	49.4	793	2 JC5831	kinesin-related pr
58	39	49.4	885	1 T04321	endopeptidase La h
59	39	49.4	921	2 T01775	hypothetical prote
60	39	49.4	928	2 T10164	kinesin heavy chai
61	39	49.4	929	2 T51932	kinesin [imported]
62	39	49.4	932	2 T30099	hypothetical prote
63	39	49.4	987	2 T51360	kinesin-like heavy
64	39	49.4	1022	2 E84792	probable kinesin h
65	39	49.4	1038	1 B42641	kinesin-related pr
66	38.5	48.7	1083	2 T26844	hypothetical prote
67	38	48.1	221	2 T06815	probable embryonic
68	38	48.1	324	2 D81452	3-oxoacyl-l-acyl-ca
69	38	48.1	325	2 S32908	hypothetical prote
70	38	48.1	330	2 B48835	kinesin-like prote
71	38	48.1	351	2 T40896	hypothetical prote
72	38	48.1	365	2 T50566	probable ABC-type
73	38	48.1	404	2 A34919	type II site-speci
74	38	48.1	692	2 T47493	hypothetical prote
75	38	48.1	718	2 A82352	iron(III) compound
76	38	48.1	857	2 E84600	probable kinesin h
77	38	48.1	873	2 JC7079	homeobox protein z
78	38	48.1	873	2 JC4863	homeobox protein z
79	38	48.1	888	2 T01081	hypothetical prote
80	38	48.1	1006	2 T02017	kinesin-related pr
81	38	48.1	1032	2 B86224	hypothetical prote
82	38	48.1	1058	2 T47525	kinesin-related pr
83	38	48.1	1076	2 B84687	probable kinesin-1
84	38	48.1	1304	2 C85188	disease resistance
85	38	48.1	1388	2 T30335	KLP2 protein - Afr
86	37	46.8	159	1 JIMS	ig J chain precurs
87	37	46.8	182	2 S33990	finger protein ZNF
88	37	46.8	329	2 S73345	sn-glycerol-3-phos
89	37	46.8	470	2 S02068	RNA-directed RNA p
90	37	46.8	507	2 T08337	hypothetical prote
91	37	46.8	575	2 T48224	probable homeodoma
92	37	46.8	596	2 AB1047	succinate dehydrog
93	37	46.8	602	1 R0BCPF	fumarate reductase
94	37	46.8	602	2 G86111	flavoprotein subun
95	37	46.8	602	2 G81270	flavoprotein subun
96	37	46.8	899	2 S76449	hypothetical prote
97	37	46.8	909	2 H86350	hypothetical prote
98	37	46.8	956	2 A71420	pyruvate, phosphat
99	37	46.8	1056	2 H84777	probable kinesin-r
100	37	46.8	1121	2 T06065	hypothetical prote
101	37	46.8	1195	2 B96746	probable kinesin T
102	37	46.8	1619	2 T18499	hypothetical prote

103	37	46.8	1893	2	T22661	hypotheoretical prote	176	35	44.3	1150	1	A55289	kinesin-like prote
104	36	45.6	101	2	T14706	probable C-type na	177	35	44.3	1225	2	A56514	chromokinesin - ch
105	36	45.6	139	2	I40783	hypotheoretical prote	178	35	44.3	1226	2	I51617	kinesin-like prote
106	36	45.6	168	2	S47467	dihydrofolate redu	179	35	44.3	1229	2	T48959	kinesin-like prote
107	36	45.6	182	2	I40175	signal peptidase I	180	35	44.3	1231	2	A54803	microtubule-asoci
108	36	45.6	199	2	A13206	transcription regu	181	35	44.3	1231	2	S28721	hypotheoretical prote
109	36	45.6	202	2	T22914	hypotheoretical prote	182	35	44.3	1650	2	A56921	kinesin family pro
110	36	45.6	204	2	A13396	hypotheoretical prote	183	35	44.3	1695	2	T39808	hypotheoretical prote
111	36	45.6	204	2	A13771	hypotheoretical prote	184	35	44.3	1958	2	T42531	acetyl-CoA carboxy
112	36	45.6	214	2	S49599	probable permease	185	35	44.3	2279	2	T42506	acetyl-CoA carboxy
113	36	45.6	248	2	H70511	probable prCA prot	186	35	44.3	2280	2	T03094	A-kinase anchor pr
114	36	45.6	265	2	E87074	proteasome [alpha]	187	35	44.3	2359	2	T18482	hypotheoretical prote
115	36	45.6	265	2	S72865	hypotheoretical prote	188	35	44.3	2437	2	AF0717	hypotheoretical prote
116	36	45.6	300	2	E71534	probable pbp2b met	189	34	43.0	56	2	TVHUSE	DNA-binding protei
117	36	45.6	330	2	E90578	30S ribosomal prot	190	34	43.0	90	2	H82343	transforming protei
118	36	45.6	344	2	T33057	hypotheoretical prote	191	34	43.0	109	1	TVHUSE	phospholipase A2 (
119	36	45.6	375	2	T08134	oleosin-like prote	192	34	43.0	139	2	JN0426	probable merf-fam
120	36	45.6	384	2	A47479	heparin lyase (EC	193	34	43.0	152	2	JN0427	lysophospholipase
121	36	45.6	401	2	C87101	probable secreted	194	34	43.0	152	2	JN0427	probable transcrip
122	36	45.6	411	1	S37643	protein kinase MSK	195	34	43.0	202	2	E95883	exotoxin 14 [impor
123	36	45.6	447	2	B64152	conserved hypothe	196	34	43.0	227	2	G98807	UDP-N-acetyl-D-man
124	36	45.6	513	2	AB2504	hypotheoretical prote	197	34	43.0	246	2	S75813	deoxyribonuclease
125	36	45.6	519	2	I54523	kinesin-related pr	198	34	43.0	260	1	B26325	deoxyribonuclease
126	36	45.6	583	2	A82430	nitrate/nitrite se	199	34	43.0	272	2	A71618	merozoite surface
127	36	45.6	622	2	A57281	kinesin-like motor	200	34	43.0	275	2	S77009	hypotheoretical prote
128	36	45.6	881	2	I84737	kinesin heavy chai	201	34	43.0	282	1	NDBOR	deoxyribonuclease
129	36	45.6	915	2	H82104	cation transport A	202	34	43.0	286	2	T09704	probable arginine/
130	36	45.6	1307	2	G96711	unknown protein, 9	203	34	43.0	290	2	T15974	hypotheoretical prote
131	36	45.6	1662	1	H71402	probable kinesin -	204	34	43.0	298	2	T22250	hypotheoretical prote
132	36	45.6	1743	2	T26859	hypotheoretical prote	205	34	43.0	302	2	E83441	conserved hypothe
133	36	45.6	1780	2	T17272	hypotheoretical prote	206	34	43.0	313	2	E82762	conserved hypothe
134	35.5	44.9	294	2	D85036	hypotheoretical prote	207	34	43.0	328	2	H81201	conserved hypothe
135	35.5	44.9	451	2	T15718	hypotheoretical prote	208	34	43.0	347	2	T06671	hypotheoretical prote
136	35	44.3	92	2	G84933	DNA-binding protei	209	34	43.0	368	2	S39198	SASP degradation s
137	35	44.3	126	2	H89826	hypotheoretical prote	210	34	43.0	372	1	A32375	L-selectin precurs
138	35	44.3	129	2	F82515	conserved hypothe	211	34	43.0	375	2	B18442	carbamoyl-phosphat
139	35	44.3	147	2	E44259	kinesin-related pr	212	34	43.0	375	2	S62606	semenclostin - mous
140	35	44.3	165	2	D86784	hypotheoretical prote	213	34	43.0	376	2	S36535	E2 protein - human
141	35	44.3	218	2	D86768	hypotheoretical prote	214	34	43.0	380	2	C90119	hypotheoretical prote
142	35	44.3	232	2	C37390	dihydrofolate redu	215	34	43.0	380	2	AG2620	hemolysin [impor
143	35	44.3	292	2	E89472	transfer protein T	216	34	43.0	384	2	G97402	hemolysin U97482 (
144	35	44.3	317	1	E87185	protein ZC53.6 [im	217	34	43.0	402	2	F82473	hypotheoretical prote
145	35	44.3	318	2	T35457	3',5'-cyclic-nucle	218	34	43.0	409	2	F70387	deoxyguanosinetrip
146	35	44.3	354	2	C96600	probable insertion	219	34	43.0	495	2	B71360	collagenase - Aqu
147	35	44.3	363	2	AE1837	protein F14J16.16	220	34	43.0	502	2	UC8025	cytochrome P450 en
148	35	44.3	372	2	JC5377	hypotheoretical prote	221	34	43.0	545	2	F64579	hypotheoretical prote
149	35	44.3	372	2	S23936	L-selectin precurs	222	34	43.0	545	2	F71932	site-specific DNA-
150	35	44.3	384	2	F96601	hypotheoretical prote	223	34	43.0	587	2	T29324	type II DNA modifi
151	35	44.3	408	2	S33683	site-specific DNA-	224	34	43.0	599	2	T18316	hypotheoretical prote
152	35	44.3	412	1	S37642	protein kinase MSK	225	34	43.0	638	2	P95399	protein [imported
153	35	44.3	463	2	D97814	chromosomal replic	226	34	43.0	666	1	A36026	kinesin-related pr
154	35	44.3	463	2	C71665	chromosomal replic	227	34	43.0	666	1	T34548	hypotheoretical prote
155	35	44.3	478	2	G90514	nadh oxidase (nox	228	34	43.0	786	2	A96956	ATP-dependent prot
156	35	44.3	493	2	S32037	finger protein XFG	229	34	43.0	875	2	T09142	endopeptidase Ia h
157	35	44.3	506	2	T08927	probable protein k	230	34	43.0	885	2	D86151	F22M8.8 protein -
158	35	44.3	529	2	A24031	genome polyprotein	231	34	43.0	893	2	T35014	probable regulator
159	35	44.3	554	2	T50118	kinesin-related pr	232	34	43.0	898	2	T21179	hypotheoretical prote
160	35	44.3	563	2	A69335	succinate dehydrog	233	34	43.0	944	2	A89624	protein F21A10.2 (
161	35	44.3	571	2	C70353	hypotheoretical prote	234	34	43.0	944	2	S26710	spindle pole body
162	35	44.3	623	2	T06704	numb-binding prote	235	34	43.0	953	2	I48078	Chol antigen - Chi
163	35	44.3	628	2	T09458	kinesin-related pr	236	34	43.0	962	1	S28262	kinesin-related pr
164	35	44.3	716	1	A44259	numb-binding prote	237	34	43.0	962	2	D70661	probable membran
165	35	44.3	728	2	T09457	kinesin-related pr	238	34	43.0	968	2	T51933	kinesin motor prot
166	35	44.3	744	2	T06048	probable lipoprote	239	34	43.0	1001	2	G87385	TonB-dependent rec
167	35	44.3	760	2	S62792	kinesin heavy chai	240	34	43.0	1233	2	T37045	nitrate reductase
168	35	44.3	843	2	G34868	pyruvate dehydrog	241	34	43.0	1285	2	H85041	hypotheoretical prote
169	35	44.3	882	2	G83018	mitotic checkpoint	242	34	43.0	1285	2	I67630	protein-tyrosine-p
170	35	44.3	1058	2	T30178	probable kinesin h	243	34	43.0	2294	2	I67630	genome polyprotein
171	35	44.3	1068	2	F84614	probable kinesin h	244	34	43.0	2332	1	GNYP	cell surface antig
172	35	44.3	1080	2	T19048	probable pro-X car	245	34	43.0	2450	2	S71625	protein-tyrosine-p
173	35	44.3	1102	2	T31004	probable mitotic c	246	34	43.0	2466	2	I67629	protein-tyrosine-p
174	35	44.3	1121	2	T13796	kinesin-related pr	247	34	43.0	2490	1	A54971	protein-tyrosine-p
175	35	44.3	1121	2	T13750	kinesin-like prote	248	34	43.0	2649	2	T51023	hypotheoretical prote

249	33.5	42.4	131	2	AG1421	hypothetical prote	322	33	41.8	566	2	C91045	nitrate/nitrite ae
250	33.5	42.4	279	2	C82915	ribosomal protei	323	33	41.8	575	2	S46692	hypothetical prote
251	33.5	42.4	323	1	S03702	L-selectin precurs	324	33	41.8	604	2	A46150	proteoglycan-endo
252	33.5	42.4	385	1	A34051	L-selectin precurs	325	33	41.8	607	2	AH0044	succinate dehydrog
253	33.5	42.4	417	2	D82172	serine transporter	326	33	41.8	611	2	T44962	hypothetical prote
254	33.5	42.4	439	2	A11388	late competence pr	327	33	41.8	632	2	T32454	hypothetical prote
255	33.5	42.4	439	2	S48273	probable transcrip	328	33	41.8	641	2	A24075	lipase precursor -
256	33.5	42.4	1208	2	AE1947	chromosome segrega	329	33	41.8	671	2	T10755	kinesin-related pr
257	33	41.8	71	2	AG2418	hypothetical prote	330	33	41.8	700	2	E69146	sensory transducti
258	33	41.8	110	1	S70466	transcription regu	331	33	41.8	707	1	A64047	ribonucleoside-tri
259	33	41.8	124	1	A70343	aspartate 1-decarb	332	33	41.8	715	2	T33573	hypothetical prote
260	33	41.8	136	2	E64067	DNA-binding protei	333	33	41.8	743	2	G83726	assimilatory nitra
261	33	41.8	137	2	T07891	protein kinase (EC	334	33	41.8	756	2	T49475	related to tol pro
262	33	41.8	139	2	S53638	protein kinase clk	335	33	41.8	771	2	S25814	hypothetical prote
263	33	41.8	142	2	H82660	plasmid stabilizat	336	33	41.8	772	2	T26330	hypothetical prote
264	33	41.8	161	2	B70323	lipopolysaccharide	337	33	41.8	802	1	A37142	outer membrane udn
265	33	41.8	198	2	G86754	prophage p12 prote	338	33	41.8	825	2	T29634	hypothetical prote
266	33	41.8	203	2	AH0223	probable glycosida	339	33	41.8	867	2	D71555	endopeptidase Clp
267	33	41.8	204	2	C83038	hypothetical prote	340	33	41.8	878	2	A55201	melosia-specific p
268	33	41.8	213	2	B25750	nodulin-26b - soyb	341	33	41.8	906	2	A82533	hypothetical prote
269	33	41.8	221	2	T29468	hypothetical prote	342	33	41.8	931	2	H86387	hypothetical prote
270	33	41.8	225	2	S50458	hypothetical prote	343	33	41.8	934	2	G91198	Gamma intimin [imp
271	33	41.8	236	2	B85025	hypothetical prote	344	33	41.8	934	2	C86045	intimin adherence
272	33	41.8	258	2	S55036	tyrosine-rich hydr	345	33	41.8	935	1	I41193	outer membrane pro
273	33	41.8	262	1	A26324	deoxyribonuclease	346	33	41.8	936	1	I40705	bacterial adhesin
274	33	41.8	265	2	T05668	pollen allergen ho	347	33	41.8	939	2	I41197	eee protein (enter
275	33	41.8	273	2	D71436	hypothetical prote	348	33	41.8	958	2	T20621	hypothetical prote
276	33	41.8	281	2	AC2138	hypothetical prote	349	33	41.8	1024	2	T34517	kinesin-related pr
277	33	41.8	284	1	JC2526	deoxyribonuclease	350	33	41.8	1073	2	S14032	kinesin-related pr
278	33	41.8	284	2	JC8053	deoxyribonuclease	351	33	41.8	1085	2	T38378	kinesin-like prote
279	33	41.8	288	2	S68798	RNA-binding protei	352	33	41.8	1089	2	T21582	hypothetical prote
280	33	41.8	290	2	A86281	protein Fl0B6.4 [i	353	33	41.8	1112	2	S49432	replicase 126K - o
281	33	41.8	312	2	PH0224	class-3 porin prot	354	33	41.8	1184	1	A34795	kinesin-related pr
282	33	41.8	313	2	JH0254	class-3 porin prot	355	33	41.8	1201	2	T00444	hypothetical prote
283	33	41.8	314	2	T43132	hypothetical prote	356	33	41.8	1210	2	A25547	ice nucleation pro
284	33	41.8	321	2	T16451	hypothetical prote	357	33	41.8	1218	2	T30447	probable helicase
285	33	41.8	322	2	AE3359	lipic acid synthe	358	33	41.8	1236	2	B36329	hypothetical prote
286	33	41.8	330	2	AG0309	probable LacI-fami	359	33	41.8	1254	2	T18277	kinesin heavy chai
287	33	41.8	331	2	A10534	hypothetical prote	360	33	41.8	1256	2	C71436	probable resistanc
288	33	41.8	337	2	AD0608	probable oxidoredu	361	33	41.8	1317	2	B85189	disease resistance
289	33	41.8	338	2	AE1119	oxidoreductase hom	362	33	41.8	1325	2	T01037	hypothetical prote
290	33	41.8	342	2	AH1479	oxidoreductase hom	363	33	41.8	1495	2	T48429	hypothetical prote
291	33	41.8	344	2	S61037	hypothetical prote	364	33	41.8	1549	2	T13940	ankyrin - fruit fl
292	33	41.8	349	2	D64825	hypothetical prote	365	33	41.8	1576	2	T29237	hypothetical prote
293	33	41.8	349	2	B90748	hypothetical prote	366	33	41.8	1584	1	JN0114	kinesin-related pr
294	33	41.8	349	2	F85598	hypothetical prote	367	33	41.8	1584	2	T15822	kinesin-like prote
295	33	41.8	360	2	S48365	hypothetical prote	368	33	41.8	1742	2	T49451	kinesin-like prote
296	33	41.8	373	2	T47115	probable 4-carboxy	369	33	41.8	1921	2	T13827	kinesin-73 - fruit
297	33	41.8	392	2	F83381	probable molybdopt	370	33	41.8	2215	2	T16871	hypothetical prote
298	33	41.8	397	2	T04206	hypothetical prote	371	33	41.8	2336	2	S37077	genome polyprotein
299	33	41.8	402	2	C71440	hypothetical prote	372	33	41.8	2467	2	D71437	probable resistanc
300	33	41.8	419	2	B49418	spermatogenesis fa	373	33	41.8	4717	2	T41581	hypothetical coile
301	33	41.8	437	2	S67679	probable membrane	374	32.5	41.1	88	2	H89858	conserved hypothet
302	33	41.8	464	2	S45363	LEO1 protein - yea	375	32.5	41.1	331	2	F85873	cell division prot
303	33	41.8	470	2	A94999	metalloelastase HM	376	32.5	41.1	331	2	E51029	cell division prot
304	33	41.8	473	2	S53119	RNA-directed RNA p	377	32.5	41.1	331	2	G65004	Div protein - Esch
305	33	41.8	482	2	H97348	NADP-dependent gly	378	32.5	41.1	352	2	T39363	RNA binding protei
306	33	41.8	493	2	G83564	probable ATPase PA	379	32.5	41.1	439	2	AC1764	late competence pr
307	33	41.8	496	2	A49418	spermatogenesis fa	380	32.5	41.1	477	2	S76496	hypothetical prote
308	33	41.8	499	2	S53637	protein kinase clk	381	32.5	41.1	718	2	A13420	penicillin-binding
309	33	41.8	507	2	T45825	hypothetical prote	382	32.5	41.1	1130	2	T30251	repetin - mouse
310	33	41.8	511	2	AH1225	cobyrlic acid synth	383	32.5	41.1	2541	2	T29340	hypothetical prote
311	33	41.8	513	2	G96757	probable protein A	384	32	40.5	42	2	A71265	hypothetical prote
312	33	41.8	527	2	AE2380	type I restriction	385	32	40.5	57	2	H72592	probable aerolysin
313	33	41.8	527	2	T41855	ACKNPV orf119 - Bo	386	32	40.5	64	2	T05933	probable 3-methyl-
314	33	41.8	534	2	S76219	hypothetical prote	387	32	40.5	67	2	AC1037	probable phage tai
315	33	41.8	542	2	JH1524	O-succinylthiomoseri	388	32	40.5	67	2	AG0927	probable phage tai
316	33	41.8	543	2	H84724	probable ARI-like	389	32	40.5	76	2	G90957	probable derepress
317	33	41.8	562	2	A44944	apical membrane an	390	32	40.5	76	2	H85805	unknown protein en
318	33	41.8	563	2	A39238	66K merozoite surf	391	32	40.5	76	2	AD2538	hypothetical prote
319	33	41.8	566	2	AD0816	nitrate/nitrite se	392	32	40.5	96	2	B75114	hypothetical prote
320	33	41.8	566	2	F85889	hypothetical prote	393	32	40.5	100	2	E83037	urease gamma subun
321	33	41.8	566	2	D65022	nitrate/nitrite se	394	32	40.5	107	2	PH0971	Ig heavy chain V r

395	32	40.5	119	2	F30502	Ig heavy chain V r	468	32	40.5	466	2	A86033	probable pernease
396	32	40.5	136	2	T03292	probable signal re	469	32	40.5	468	2	T08139	shaggy-like protei
397	32	40.5	136	2	T46345	hypothetical prote	470	32	40.5	472	1	T01236	serine/threonine-s
398	32	40.5	137	2	H32513	Ig heavy chain pre	471	32	40.5	475	2	T12955	probable protein k
399	32	40.5	137	2	T49243	hypothetical prote	472	32	40.5	477	2	JE0343	tef protein - rat
400	32	40.5	138	2	B70941	hypothetical prote	473	32	40.5	485	2	E81871	probable GTP-bind
401	32	40.5	149	2	H70441	ribosomal protein	474	32	40.5	485	2	G81149	essential GTPase N
402	32	40.5	152	2	A10448	probable ribonucle	475	32	40.5	491	2	I40455	penicillin binding
403	32	40.5	159	2	B70063	hypothetical prote	476	32	40.5	505	2	C69666	NADH dehydrogenase
404	32	40.5	177	2	F96739	hypothetical prote	477	32	40.5	511	1	B34160	cytochrome P450 4A
405	32	40.5	188	2	H81066	hypothetical prote	478	32	40.5	515	2	JC1525	alpha-1B-adrenergi
406	32	40.5	191	2	G81268	50S ribosomal prot	479	32	40.5	517	2	A45121	alpha-1B adrenergi
407	32	40.5	196	2	S41281	ribosomal protein	480	32	40.5	523	2	A53196	orphan hormone nuc
408	32	40.5	196	2	S41282	ribosomal protein	481	32	40.5	527	1	S69203	teichoic acid tran
409	32	40.5	196	2	S41254	ribosomal protein	482	32	40.5	532	2	JC6170	GATA-transcription
410	32	40.5	196	2	S41255	ribosomal protein	483	32	40.5	534	2	T01500	cytokinin oxidase
411	32	40.5	196	2	S41266	ribosomal protein	484	32	40.5	534	2	T51929	cytokinin oxidase
412	32	40.5	196	2	S41278	ribosomal protein	485	32	40.5	547	2	A56575	puff-specific nucl
413	32	40.5	196	2	S41276	ribosomal protein	486	32	40.5	562	2	JU0033	hypothetical L1 pr
414	32	40.5	196	2	S41283	ribosomal protein	487	32	40.5	571	2	S49119	embryonic/neonatal
415	32	40.5	196	2	S41284	ribosomal protein	488	32	40.5	574	2	S73730	MG307 homolog H08
416	32	40.5	199	2	T23484	hypothetical prote	489	32	40.5	577	2	B83388	probable carbamoyl
417	32	40.5	201	1	R3R24	ribosomal protein	490	32	40.5	577	2	D97337	mismatch repair pr
418	32	40.5	201	1	R32M4	ribosomal protein	491	32	40.5	585	2	T31077	probable ABC-trans
419	32	40.5	201	1	H85910	unknown protein en	492	32	40.5	595	2	D83007	regulatory protein
420	32	40.5	216	2	D97315	metallo-beta-lacta	493	32	40.5	605	2	B86461	probable protein k
421	32	40.5	233	2	H97094	hypothetical prote	494	32	40.5	614	2	A86094	diphosphate-fructo
422	32	40.5	237	2	S55614	hypothetical prote	495	32	40.5	616	2	JC7892	acyl-CoA dehydroge
423	32	40.5	244	2	T15996	hypothetical prote	496	32	40.5	621	2	J49199	growth factor rece
424	32	40.5	244	2	T41030	hypothetical prote	497	32	40.5	622	2	E83160	two-component sens
425	32	40.5	257	2	S56815	hypothetical prote	498	32	40.5	625	2	S69707	hypothetical prote
426	32	40.5	263	2	F82311	hypothetical prote	499	32	40.5	640	2	A64065	hypothetical prote
427	32	40.5	263	2	AF0420	survival protein S	500	32	40.5	648	2	AF2257	hypothetical prote
428	32	40.5	266	2	T02807	phosphonates trans	501	32	40.5	666	2	T22943	hypothetical prote
429	32	40.5	268	2	S03328	arsenate reductase	502	32	40.5	668	2	T02791	mitotic centromere
430	32	40.5	268	2	S04135	embryonic abundant	503	32	40.5	673	2	S60173	fragile X mental r
431	32	40.5	268	2	S04136	embryonic abundant	504	32	40.5	693	2	S46417	heat shock protein
432	32	40.5	268	2	S05471	embryonic abundant	505	32	40.5	695	2	G85135	hypothetical prote
433	32	40.5	268	2	S14068	seed protein precu	506	32	40.5	700	1	S09748	kinesin-related pr
434	32	40.5	274	2	D95339	hypothetical prote	507	32	40.5	705	2	T01730	hypothetical prote
435	32	40.5	287	2	A27082	2,4-dichlorophenox	508	32	40.5	707	1	LEEBBV	hemolysin secretio
436	32	40.5	290	2	T24747	hypothetical prote	509	32	40.5	713	2	A12514	ABC transporter AT
437	32	40.5	296	2	T29923	hypothetical prote	510	32	40.5	714	2	D85014	hypothetical prote
438	32	40.5	302	2	AC2225	hypothetical prote	511	32	40.5	720	2	H95221	alpha-galactosidas
439	32	40.5	305	2	S77397	yabc protein homol	512	32	40.5	720	2	G98085	alpha-galactosidas
440	32	40.5	308	1	G64306	glutaminase homolo	513	32	40.5	725	2	S57127	hypothetical prote
441	32	40.5	308	2	C90895	probable glutamina	514	32	40.5	747	2	T23607	probable membrane
442	32	40.5	308	2	E85722	probable glutamina	515	32	40.5	755	2	E97080	hypothetical prote
443	32	40.5	309	2	T15696	hypothetical prote	516	32	40.5	757	2	AC2691	uVRA-like protein,
444	32	40.5	326	2	B88979	peroxidase homolog	517	32	40.5	757	2	G97472	penicillin binding
445	32	40.5	331	2	S76480	protein F37B4.10 [518	32	40.5	768	2	T37601	penicillin-binding
446	32	40.5	341	2	A47083	hypothetical prote	519	32	40.5	781	2	T39373	probable transcript
447	32	40.5	342	2	AH1045	hypothetical prote	520	32	40.5	788	2	C82595	dynamain-related pr
448	32	40.5	342	2	T26677	conserved hypotet	521	32	40.5	826	2	C96694	ferric enterobacti
449	32	40.5	348	2	AG1161	hypothetical prote	522	32	40.5	875	2	AB1125	hypothetical prote
450	32	40.5	351	2	S39603	hypothetical prote	523	32	40.5	931	2	B75027	E. coli YbgG protei
451	32	40.5	351	2	S74846	class I histocompa	524	32	40.5	935	2	T51930	hypothetical prote
452	32	40.5	358	1	A28630	hypothetical prote	525	32	40.5	959	1	B71405	kinesin [imported]
453	32	40.5	375	1	E64674	muconate cyclisom	526	32	40.5	990	2	T12678	probable kinesin -
454	32	40.5	375	2	T35015	carbamoyl-phosphat	527	32	40.5	1000	1	A33620	hypothetical prote
455	32	40.5	376	2	JC4892	probable 3-oxoadip	528	32	40.5	1000	1	C82630	myosin heavy chain
456	32	40.5	387	2	A47287	L-selectin precurs	529	32	40.5	1011	2	S45573	serine proteinase
457	32	40.5	391	2	B97008	estradiol 17beta-d	530	32	40.5	1011	2	S45573	myosin IA - fruit
458	32	40.5	401	2	T18661	cyclopropane fatty	531	32	40.5	1013	2	T33470	probable kinesin -
459	32	40.5	411	2	T17750	hypothetical prote	532	32	40.5	1025	2	T45811	hypothetical prote
460	32	40.5	423	2	T48121	hypothetical prote	533	32	40.5	1066	1	A48669	Ga2+-transporting
461	32	40.5	423	2	T51794	hypothetical prote	534	32	40.5	1066	1	A42640	kinesin-related pr
462	32	40.5	433	2	A35557	MYB DNA-binding-l1	535	32	40.5	1111	1	A33284	myosin heavy chain
463	32	40.5	442	2	T47750	N2,N2-dimethylguan	536	32	40.5	1130	2	A48843	MHC class II trans
464	32	40.5	463	2	G97300	myosin heavy chain	537	32	40.5	1132	2	D98250	protein t21B10.3 [
465	32	40.5	463	2	G97300	aspartyl/asparagin	538	32	40.5	1133	1	S43938	endopeptidase La-1
466	32	40.5	464	2	T40108	glucan 1,3-beta-gl	539	32	40.5	1153	1	RWHU1B	cell surface glyco
467	32	40.5	466	2	B91186	probable pernease	540	32	40.5	1170	2	T25043	hypothetical prote

probable pernease
shaggy-like protei
serine/threonine-s
probable protein k
tef protein - rat
probable GTP-bind
essential GTPase N
penicillin binding
NADH dehydrogenase
cytochrome P450 4A
alpha-1B-adrenergi
alpha-1B adrenergi
orphan hormone nuc
teichoic acid tran
GATA-transcription
cytokinin oxidase
cytokinin oxidase
puff-specific nucl
hypothetical L1 pr
embryonic/neonatal
MG307 homolog H08
probable carbamoyl
mismatch repair pr
probable ABC-trans
regulatory protein
probable protein k
diphosphate-fructo
acyl-CoA dehydroge
growth factor rece
two-component sens
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
mitotic centromere
fragile X mental r
heat shock protein
hypothetical prote
kinesin-related pr
hypothetical prote
hemolysin secretio
ABC transporter AT
hypothetical prote
alpha-galactosidas
alpha-galactosidas
hypothetical prote
probable membrane
hypothetical prote
uVRA-like protein,
penicillin binding
penicillin-binding
probable transcript
dynamain-related pr
ferric enterobacti
hypothetical prote
E. coli YbgG protei
hypothetical prote
kinesin [imported]
probable kinesin -
hypothetical prote
myosin heavy chain
serine proteinase
myosin IA - fruit
myosin IA - fruit
Ga2+-transporting
kinesin-related pr
kinesin-related pr
MHC class II trans
protein t21B10.3 [
endopeptidase La-1
cell surface glyco
hypothetical prote

541	32	40.5	1321	2	T13283	probable transcrip	614	31	39.2	211	2	C84751	hypothetical prote
542	32	40.5	1358	2	T29041	hypothetical prote	615	31	39.2	216	2	T26505	hypothetical prote
543	32	40.5	1389	2	T41230	hypothetical tpr d	616	31	39.2	221	2	S70755	conserved hypotet
544	32	40.5	1459	2	A12488	hypothetical prote	617	31	39.2	224	2	G89890	hypothetical prote
545	32	40.5	1532	2	T18438	hypothetical prote	618	31	39.2	224	2	T47397	hypothetical prote
546	32	40.5	1567	2	S11672	ice nucleation pro	619	31	39.2	227	2	S77870	dnak-type molecula
547	32	40.5	1784	2	T43167	sodium channel pro	620	31	39.2	230	2	C86141	protein T25K16.5 (
548	32	40.5	1937	2	I38055	myosin heavy chain	621	31	39.2	233	2	E89976	conserved hypotet
549	32	40.5	1938	1	A09997	myosin heavy chain	622	31	39.2	236	2	E89090	conserved hypotet
550	32	40.5	1938	1	S06005	myosin alpha heavy	623	31	39.2	236	2	T19789	hypothetical prote
551	32	40.5	1938	1	JK0178	myosin heavy chain	624	31	39.2	242	2	T48581	hypothetical prote
552	32	40.5	1938	2	A59293	skeletal myosin he	625	31	39.2	243	2	T28802	hypothetical prote
553	32	40.5	1938	2	I49464	alpha cardiac myos	626	31	39.2	249	2	S39698	nitro/flavin reduc
554	32	40.5	1939	1	A46762	myosin alpha heavy	627	31	39.2	256	2	B75079	hypothetical prote
555	32	40.5	1939	2	I48175	myosin heavy chain	628	31	39.2	262	2	A13518	nitrate reductase
556	32	40.5	1940	1	A24922	myosin heavy chain	629	31	39.2	263	2	AC0522	probable secreted
557	32	40.5	1940	1	S04090	myosin heavy chain	630	31	39.2	271	2	T47119	3-methyl-2-oxobuta
558	32	40.5	1940	2	A29320	myosin heavy chain	631	31	39.2	277	2	T05091	probable methyltra
559	32	40.5	1940	2	A59287	myosin heavy chain	632	31	39.2	280	2	AC3579	transcription regu
560	32	40.5	1974	2	T30010	hypothetical prote	633	31	39.2	284	1	S12676	deoxyribonuclease
561	32	40.5	1992	1	S02771	myosin heavy chain	634	31	39.2	295	2	T27475	hypothetical prote
562	32	40.5	2186	2	T13169	tiggrin - fruit fl	635	31	39.2	296	2	T06572	convicillin precurs
563	32	40.5	2332	1	GNV4F	genome polypeptide	636	31	39.2	301	2	S78543	drdp-4-dehydroxam
564	32	40.5	2539	2	B71619	hypothetical prote	637	31	39.2	301	2	S78543	protein P28J9.4 [1
565	32	40.5	2555	2	A40043	hypothetical prote	638	31	39.2	301	2	T51435	hypothetical prote
566	32	40.5	2592	2	D23768	notch protein homo	639	31	39.2	301	2	T01193	reverse transcript
567	32	40.5	6669	2	S55024	hypothetical prote	640	31	39.2	313	2	E83095	conserved hypotet
568	31.5	39.9	77	2	F95154	nebulin, skeletal	641	31	39.2	313	2	AE2812	conserved hypotet
569	31.5	39.9	346	2	D75303	hypothetical prote	642	31	39.2	315	2	A70313	NADH2 dehydrogenas
570	31.5	39.9	378	2	AE0484	conserved hypotet	643	31	39.2	322	2	H90057	conserved hypotet
571	31.5	39.9	379	2	S74601	probable glycerate	644	31	39.2	324	2	T18818	hypothetical prote
572	31.5	39.9	392	2	D64493	hypothetical prote	645	31	39.2	338	2	S75196	hypothetical prote
573	31.5	39.9	472	2	A33275	nonspecific lipid-	646	31	39.2	338	2	S56533	hypothetical prote
574	31.5	39.9	473	2	T19707	glycosomal protein	647	31	39.2	338	2	T43440	hypothetical 38K p
575	31.5	39.9	495	2	F83213	hypothetical prote	648	31	39.2	340	2	T27389	hypothetical prote
576	31.5	39.9	526	2	S48663	conserved hypotet	649	31	39.2	342	2	G96618	probable proline-r
577	31.5	39.9	540	2	S44830	phosphoenolpyruvat	650	31	39.2	343	2	A84335	chloromuconate cyc
578	31.5	39.9	788	1	I52822	F54P2.5 protein -	651	31	39.2	346	2	F37590	probable reductase
579	31	39.2	48	2	ABJ386	diacylglycerol kin	652	31	39.2	350	2	S44717	hypothetical prote
580	31	39.2	51	2	T41535	hypothetical prote	653	31	39.2	352	2	AH2039	hypothetical prote
581	31	39.2	58	1	WMTM68	60S ribosomal prot	654	31	39.2	354	2	S44724	outer membrane pro
582	31	39.2	63	2	T13265	6.8K protein - tob	655	31	39.2	355	2	G84904	probable DOP zinc
583	31	39.2	90	2	S35438	Cro repressor prot	656	31	39.2	365	2	A98088	membrane-bound lyl
584	31	39.2	90	2	S62081	DNA-binding protei	657	31	39.2	365	2	A65084	membrane-bound lyl
585	31	39.2	100	2	B40651	M-like protein pre	658	31	39.2	365	2	C85933	membrane-bound lyl
586	31	39.2	112	2	S51121	hypothetical prote	659	31	39.2	365	2	AD2811	conserved hypotet
587	31	39.2	116	2	C72731	genome polypeptide	660	31	39.2	368	2	C29356	hydroxyproline-ric
588	31	39.2	121	2	F69891	hypothetical prote	661	31	39.2	375	2	E70011	potassium channel
589	31	39.2	139	2	I40604	conserved hypotet	662	31	39.2	376	2	F81224	glycosyltransferas
590	31	39.2	142	2	C70059	hypothetical prote	663	31	39.2	377	2	A81996	glycosyltransferas
591	31	39.2	143	2	H83935	hypothetical prote	664	31	39.2	382	2	AH2056	hypothetical prote
592	31	39.2	144	2	T12102	hypothetical prote	665	31	39.2	385	2	A40359	aliphatic amidase
593	31	39.2	145	2	F69214	glycine-rich prote	666	31	39.2	385	2	C83226	aliphatic amidase
594	31	39.2	152	2	D71569	heat shock protein	667	31	39.2	387	2	S61615	hypothetical prote
595	31	39.2	166	2	T25773	probable hth trans	668	31	39.2	389	2	A55433	hypothetical prote
596	31	39.2	173	2	T08011	hypothetical prote	669	31	39.2	401	2	T42655	oxytocin receptor
597	31	39.2	176	2	S52914	2S seed storage pr	670	31	39.2	405	2	A83781	hypothetical prote
598	31	39.2	181	2	S44765	virion protein j13	671	31	39.2	405	2	D83826	transposase (01) B
599	31	39.2	182	2	C90936	C29E4.9 protein -	672	31	39.2	405	2	A84042	transposase (01) B
600	31	39.2	182	2	G85784	hypothetical prote	673	31	39.2	405	2	T06767	probable transcrip
601	31	39.2	182	2	A64935	hypothetical prote	674	31	39.2	409	2	T35598	hypothetical prote
602	31	39.2	183	2	S52904	hypothetical prote	675	31	39.2	412	2	G69330	hypothetical prote
603	31	39.2	184	2	E72700	virion protein j13	676	31	39.2	412	2	S48881	isocitrate dehydro
604	31	39.2	185	2	S52903	hypothetical prote	677	31	39.2	412	2	S50963	rRNA (guanosine-2'
605	31	39.2	186	2	S28021	virion protein j13	678	31	39.2	415	2	B84858	hypothetical prote
606	31	39.2	189	2	S52902	rabi8 protein - Ar	679	31	39.2	417	2	F96607	hypothetical prote
607	31	39.2	189	2	S52907	virion protein j13	680	31	39.2	417	2	E90844	probable clathrin-
608	31	39.2	189	2	S59399	hypothetical prote	681	31	39.2	417	2	H83708	probable factor [1
609	31	39.2	191	2	S52909	hypothetical prote	682	31	39.2	417	2	D85702	hypothetical prote
610	31	39.2	193	2	A82419	virion protein j13	683	31	39.2	417	2	A64869	hypothetical prote
611	31	39.2	196	2	S52906	conserved hypotet	684	31	39.2	422	2	A83184	ychp protein - Bac
612	31	39.2	208	2	G64416	virion protein j13	685	31	39.2	422	2	T22732	probable protein m
613	31	39.2	210	2	D87394	hypothetical prote	686	31	39.2	425	2	H90415	hypothetical prote

687	31	39.2	428	1	I36930	involucrin - white	760	31	39.2	632	2	T18692	hypothetical prote
688	31	39.2	431	1	E70699	probable pkaA prot	761	31	39.2	635	2	C81861	hypothetical prote
689	31	39.2	440	2	C96014	probable sugar upt	762	31	39.2	637	2	S74677	hypothetical prote
690	31	39.2	440	2	C34332	glutelin 3 precurs	763	31	39.2	649	2	F88651	protein B0212.1 [i
691	31	39.2	441	2	F83683	transposase (01) B	764	31	39.2	661	2	A55877	tumor necrosis fac
692	31	39.2	449	2	T51720	glucose-6-phosphat	765	31	39.2	663	2	S21912	BRcore-Q1-21 prote
693	31	39.2	455	2	C97256	uncharacterized pr	766	31	39.2	664	2	S02116	RNA helicase WS11
694	31	39.2	457	2	C85434	glucosyltransferas	767	31	39.2	670	2	C83540	conserved hypothet
695	31	39.2	458	2	F97589	hypothetical prote	768	31	39.2	684	2	A97679	peptidyl-di-peptida
696	31	39.2	460	2	G90035	Tcaa protein [limpo	769	31	39.2	686	2	AG2303	conserved hypothet
697	31	39.2	460	2	AF1945	ParA family protei	770	31	39.2	687	2	A86402	protein T22C5.17 [
698	31	39.2	462	1	YKPHB	semenogelin I prec	771	31	39.2	704	2	S21911	BRcore-NS-23 prote
699	31	39.2	464	1	YKPG	citrate (sil)-synth	772	31	39.2	711	2	S73898	DNA topoisomerase
700	31	39.2	468	2	JC5417	phosphoprotein pho	773	31	39.2	715	2	H84799	hypothetical prote
701	31	39.2	470	2	JN0431	RNA-directed RNA p	774	31	39.2	728	2	S21913	BRcore-TN11-Q1-21
702	31	39.2	471	1	S08325	flavonol 3-O-glucu	775	31	39.2	732	1	HVHUK	probable transport
703	31	39.2	471	1	S01052	flavonol 3-O-glucu	776	31	39.2	741	2	H85589	probable transport
704	31	39.2	471	2	S01037	flavonol 3-O-glucu	777	31	39.2	762	2	E81371	probable periplasm
705	31	39.2	472	2	A86347	branched-chain alp	778	31	39.2	769	2	F89870	serine proteinase
706	31	39.2	472	2	T51858	hypothetical prote	779	31	39.2	772	2	T43034	kinesin-like prote
707	31	39.2	472	2	T23534	melibiose carrier	780	31	39.2	775	2	T43033	kinesin-like prote
708	31	39.2	476	2	AC1023	ORD protein - frui	781	31	39.2	775	2	T43033	probable membrane
709	31	39.2	476	2	S23576	glutelin 22 precu	782	31	39.2	786	2	H64817	similar to mammali
710	31	39.2	479	2	S66578	glutelin - rice	783	31	39.2	794	2	D84765	kinesin-like prote
711	31	39.2	495	2	S18745	hypothetical prote	784	31	39.2	813	2	T46242	hypothetical prote
712	31	39.2	496	2	S43776	NADPH-ferrihemopro	785	31	39.2	815	2	T41490	kinesin-like prote
713	31	39.2	506	2	S37156	Rieske [2Fe-2S] ir	786	31	39.2	817	2	T50240	hypothetical prote
714	31	39.2	508	2	G84133	permease of the Na	787	31	39.2	823	2	T21943	hypothetical prote
715	31	39.2	513	2	F96943	BRcore-Z protein -	788	31	39.2	825	2	T21943	hypothetical prote
716	31	39.2	514	2	S21914	spindle pole body-	789	31	39.2	830	2	AX0517	myosin s-1 heavy c
717	31	39.2	514	2	A57280	hypothetical prote	790	31	39.2	882	2	F84029	tpoC protein homol
718	31	39.2	517	2	T02464	butyrophilin precu	791	31	39.2	887	2	E82097	valyl-tRNA synthet
719	31	39.2	526	2	S70587	butyrophilin - bov	792	31	39.2	887	2	S43196	protein-P-II uridy
720	31	39.2	526	2	T37821	chromosomal replic	793	31	39.2	890	2	AH0528	[protein-P-II] urid
721	31	39.2	532	2	A13494	gene ND5 intron 1	794	31	39.2	890	2	G64740	[protein-P-II] urid
722	31	39.2	533	2	S10841	homeotic protein b	795	31	39.2	890	2	A85501	protein PII-uridyl
723	31	39.2	538	1	S12570	zinc finger 2 prote	796	31	39.2	890	2	A90650	probable proline-r
724	31	39.2	540	2	S57785	ND5 intron 2 prote	797	31	39.2	890	2	A90650	probable DNA repai
725	31	39.2	544	2	S09143	glutamate-tRNA lig	798	31	39.2	891	2	G84693	hypothetical prote
726	31	39.2	552	2	S65787	probable AMP-bindi	799	31	39.2	897	2	T37813	hypothetical prote
727	31	39.2	553	2	B69167	hypothetical prote	800	31	39.2	906	2	AG1957	[protein-P-II] urid
728	31	39.2	555	2	A83327	hypothetical prote	801	31	39.2	912	2	AG1957	hemoglobin-binding
729	31	39.2	555	2	T26413	30S ribosomal prot	802	31	39.2	953	2	B64083	probable membrane
730	31	39.2	559	2	C83250	30S ribosomal prot	803	31	39.2	1009	2	S20538	chitin synthase (E
731	31	39.2	561	2	G81842	30S ribosomal prot	804	31	39.2	1021	2	T15765	chitin synthase (E
732	31	39.2	561	2	G81099	hypothetical prote	805	31	39.2	1026	2	T18220	probable maturase
733	31	39.2	567	2	T16105	acetate-CoA ligase	806	31	39.2	1035	2	S78139	probable complemen
734	31	39.2	567	2	AF3611	hypothetical prote	807	31	39.2	1053	2	S46139	probable polyprote
735	31	39.2	569	2	T17779	hypothetical prote	808	31	39.2	1054	2	G85079	hemoglobin-binding
736	31	39.2	571	2	S00566	convicilin precurs	809	31	39.2	1084	2	B64088	hypothetical prote
737	31	39.2	580	2	AG1342	mannose-6-phosphat	810	31	39.2	1110	2	T29327	hypothetical prote
738	31	39.2	582	2	T16104	hypothetical prote	811	31	39.2	1113	2	T47381	probable polyprote
739	31	39.2	582	2	RNEGB1	DNA-directed RNA p	812	31	39.2	1138	2	G85077	probable DNA-direc
740	31	39.2	586	1	RNEGB1	asparagine synthas	813	31	39.2	1144	2	A81983	probable DNA-polymerase III
741	31	39.2	594	2	T02978	hypothetical ABC e	814	31	39.2	1144	2	H81037	DNA polymerase III
742	31	39.2	596	2	S72638	fumarate reductase	815	31	39.2	1164	2	T03814	tumor suppressor p
743	31	39.2	598	1	RDEBFV	NADH2 dehydrogenas	816	31	39.2	1166	2	F90247	reverse gyrase (co
744	31	39.2	598	2	AG0311	NADH2 dehydrogenas	817	31	39.2	1171	2	A42916	metabotropic gluta
745	31	39.2	600	1	D65000	NADH2 dehydrogenas	818	31	39.2	1171	2	T42372	probable guanylate
746	31	39.2	600	2	AD0797	NADH dehydrogenase	819	31	39.2	1171	2	A42916	metabotropic gluta
747	31	39.2	600	2	C85869	NADH dehydrogenase	820	31	39.2	1180	2	JC21132	protein-tyrosine-p
748	31	39.2	600	2	B91025	ribophorin I precu	821	31	39.2	1187	1	JC21132	protein-tyrosine-p
749	31	39.2	605	2	A27274	hypothetical prote	822	31	39.2	1189	1	UC4155	probable chromosom
750	31	39.2	605	2	T04197	hypothetical prote	823	31	39.2	1194	2	T37503	hypothetical prote
751	31	39.2	605	2	T26088	terminal protein p	824	31	39.2	1201	2	E86402	hypothetical prote
752	31	39.2	606	1	UZAD12	ribophorin I precu	825	31	39.2	1201	2	JC2131	metabotropic gluta
753	31	39.2	607	2	A26168	hemagglutinin - ri	826	31	39.2	1215	2	E84480	probable retroelem
754	31	39.2	609	1	HMN2KA	hemagglutinin - ri	827	31	39.2	1215	2	E84480	probable retroelem
755	31	39.2	609	2	S43009	probable ATP-depen	828	31	39.2	1256	2	F88886	protein P52G2.2 [i
756	31	39.2	613	2	F64056	hypothetical prote	829	31	39.2	1265	2	F88886	leukocyte common a
757	31	39.2	615	2	B86713	ABC transporter, A	830	31	39.2	1273	1	TDR1LT	hypothetical prote
758	31	39.2	619	2	F82391	DNA mismatch repai	831	31	39.2	1305	2	H96559	hypothetical prote
759	31	39.2	623	2	AI3637		832	31	39.2	1312	2	D85066	

833	31	39.2	1314	2	T47331	hypothetical prote	906	30	38.0	149	2	F72153	P4R protein - vari
834	31	39.2	1388	2	T47961	hypothetical prote	907	30	38.0	149	2	D36839	C4R protein - vari
835	31	39.2	1472	2	A84470	hypothetical prote	908	30	38.0	150	2	S50063	probable endonucle
836	31	39.2	1485	1	IS2FT2	DNA topoisomerase	909	30	38.0	151	2	D86638	conserved hypothet
837	31	39.2	1643	2	T07961	myosin heavy chain	910	30	38.0	154	2	S55630	hypothetical prote
838	31	39.2	1648	2	S57163	probable membrane	911	30	38.0	157	2	I47153	transcription fact
839	31	39.2	1756	2	T02599	hypothetical prote	912	30	38.0	157	2	B46243	epidermal growth f
840	31	39.2	1767	2	T00458	hypothetical prote	913	30	38.0	161	2	A00836	probable bacteriop
841	31	39.2	1770	2	S69953	hypothetical prote	914	30	38.0	161	2	AD0930	probable phage tai
842	31	39.2	1887	2	C86478	Tyb protein - yeas	915	30	38.0	161	2	AG1034	probable phage tai
843	31	39.2	1911	2	T43048	protein F1504.13 [916	30	38.0	161	2	D86418	unknown protei
844	31	39.2	1970	2	T03284	calcium channel al	917	30	38.0	162	2	H83459	C-type
845	31	39.2	2121	2	A59233	myoblast city prot	918	30	38.0	167	2	A37246	myelin basic prote
846	31	39.2	2248	2	A59338	myosin VII-like pr	919	30	38.0	175	2	T50968	hypothetical prote
847	31	39.2	3924	2	S37431	profilaggrin - hum	920	30	38.0	176	2	S50822	bZIP protein - whe
848	30.5	38.6	174	2	D86852	ankyrin 2, neuroa	921	30	38.0	179	2	G84477	hypothetical prote
849	30.5	38.6	193	2	S16399	hypothetical prote	922	30	38.0	179	2	AH2835	soluble lytic tran
850	30.5	38.6	264	1	E70027	papJ protein precu	923	30	38.0	185	2	AF2073	hypothetical prote
851	30.5	38.6	299	2	T12483	probable 3-oxoacyl	924	30	38.0	186	2	T47428	hypothetical prote
852	30.5	38.6	392	1	A37157	hypothetical prote	925	30	38.0	188	2	F69262	hypothetical prote
853	30.5	38.6	412	2	T34415	3-methyl-2-oxobuta	926	30	38.0	192	2	G89756	hypothetical prote
854	30.5	38.6	596	2	B87112	hypothetical prote	927	30	38.0	195	2	C97613	probable transglyc
855	30.5	38.6	755	2	A12174	conserved hypothet	928	30	38.0	197	2	AE2120	cytochrome c oxida
856	30.5	38.6	995	2	T05842	penicillin-binding	929	30	38.0	197	2	I50469	RAG-1 protein - sa
857	30.5	38.6	1039	2	T22982	hypothetical prote	930	30	38.0	198	2	A70013	sulfite oxidase ho
858	30.5	38.6	1180	2	T20773	hypothetical prote	931	30	38.0	200	2	A44762	outer membrane pro
859	30.5	38.6	1192	2	H86293	hypothetical prote	932	30	38.0	202	1	A44247	C4b-binding protei
860	30.5	38.6	1525	1	GNWVS5	protein F59B10.1 [933	30	38.0	203	2	AG2120	hypothetical prote
861	30.5	38.6	4549	2	T20771	genome polyprotein	934	30	38.0	207	2	T08109	oleosin-like prote
862	30.5	38.6	4667	2	T20774	hypothetical prote	935	30	38.0	207	2	E86429	hypothetical prote
863	30	38.0	20	2	S68617	hypothetical prote	936	30	38.0	212	2	H75277	hypothetical prote
864	30	38.0	49	2	T07307	histone H2A - sea	937	30	38.0	213	2	A21177	Ig light chain pre
865	30	38.0	55	2	B70120	hypothetical prote	938	30	38.0	215	2	H87602	Ig light chain pre
866	30	38.0	62	2	A34326	hypothetical prote	939	30	38.0	216	2	T10254	flagellin modifca
867	30	38.0	63	2	D95169	protamine - chicke	940	30	38.0	220	2	T28639	S11 protein, self-
868	30	38.0	65	1	GACH	hypothetical prote	941	30	38.0	222	2	AE1164	y4JL protein - Rhi
869	30	38.0	66	2	H95110	protamine - chicke	942	30	38.0	223	2	S44974	transglycosylase h
870	30	38.0	66	2	F97979	ribosomal protein	943	30	38.0	223	2	AE1523	lmbu protein - Str
871	30	38.0	67	2	T44077	50S ribosomal prot	944	30	38.0	229	1	Q3SAEC	transglycosylase h
872	30	38.0	71	2	D82155	hypothetical prote	945	30	38.0	231	2	B49934	replication initia
873	30	38.0	76	2	B72173	hypothetical prote	946	30	38.0	231	2	D89807	phosphoglycolate p
874	30	38.0	81	2	D82631	H11R protein - var	947	30	38.0	232	2	G89025	exotoxin 11 [impor
875	30	38.0	86	2	T28871	hypothetical prote	948	30	38.0	233	2	F64482	protein F13A2.8 [i
876	30	38.0	90	1	DNECS2	hypothetical prote	949	30	38.0	233	2	AF3522	hypothetical prote
877	30	38.0	90	2	AH0931	DNA-binding protei	950	30	38.0	243	2	S27758	transcription regu
878	30	38.0	90	2	C91244	histone like DNA-b	951	30	38.0	243	2	G86701	maturational-associ
879	30	38.0	90	2	A86092	DNA-binding protei	952	30	38.0	245	2	AE3517	hypothetical prote
880	30	38.0	90	2	A31388	DNA-binding protei	953	30	38.0	245	2	S43774	3-oxoacyl-(acyl-ca
881	30	38.0	91	2	AC0454	DNA-binding protei	954	30	38.0	245	2	D86780	S11 protein - Chac
882	30	38.0	94	2	A84966	DNA-binding protei	955	30	38.0	245	2	H91014	glycerol uptake fa
883	30	38.0	100	2	AD1410	integration host f	956	30	38.0	245	2	B85859	heme exporter prot
884	30	38.0	100	2	AC1786	cellobiose phospho	957	30	38.0	245	2	E64989	heme exporter prot
885	30	38.0	102	2	S73743	cellobiose phospho	958	30	38.0	250	2	T16631	heme exporter prot
886	30	38.0	103	2	B26167	hypothetical prote	959	30	38.0	251	2	A84019	NADPH-flavin oxido
887	30	38.0	106	2	I50584	Ig lambda chain C	960	30	38.0	251	2	S75353	hypothetical prote
888	30	38.0	107	2	D83918	RAG-1 protein - nu	961	30	38.0	253	2	T33533	hypothetical prote
889	30	38.0	108	2	AH0176	hypothetical prote	962	30	38.0	254	2	D69789	hypothetical prote
890	30	38.0	117	2	S01822	probable sulfite r	963	30	38.0	256	2	T48588	hypothetical prote
891	30	38.0	117	2	E71899	Ig heavy chain V-D	964	30	38.0	257	2	AE3190	3-oxoacyl-(acyl-ca
892	30	38.0	119	2	A69881	hypothetical prote	965	30	38.0	259	2	S56646	chaperonin 60 beta
893	30	38.0	119	2	AC2351	conserved hypothet	966	30	38.0	260	2	C56827	protein F20B17.2 [
894	30	38.0	123	2	A97138	hypothetical prote	967	30	38.0	263	2	A81197	DNA repair protein
895	30	38.0	124	2	T39810	uncharacterized pr	968	30	38.0	263	2	G83738	transcription regu
896	30	38.0	125	1	HSUR9M	hypothetical prote	969	30	38.0	264	2	A81834	DNA repair protein
897	30	38.0	132	2	H59093	histone H2A, gonad	970	30	38.0	266	2	I49050	Ly-49E-GE antigen
898	30	38.0	132	2	T46905	hypothetical prote	971	30	38.0	266	2	I49051	Ly-49F-GE antigen
899	30	38.0	137	2	S68956	hypothetical prote	972	30	38.0	274	2	T05769	myb-related protei
900	30	38.0	138	2	AH0100	nucleoside-diphosp	973	30	38.0	278	2	B69663	formamidopyrimidin
901	30	38.0	141	2	H64909	hypothetical prote	974	30	38.0	278	2	T39517	dual-specificity M
902	30	38.0	147	2	A53180	yfdo protein - Esc	975	30	38.0	280	2	A98934	hypothetical prote
903	30	38.0	147	2	C64223	ribonuclease PL3 (976	30	38.0	280	2	E85782	hypothetical prote
904	30	38.0	149	1	WMVZK7	hypothetical prote	977	30	38.0	280	2	S10873	regulatory protein
905	30	38.0	149	2	T28462	K7 protein 28R - v	978	30	38.0	282	1	NDHU1	deoxyribonuclease

979 30 38.0 284 2 T23636
980 30 38.0 285 2 C64750
981 30 38.0 286 2 S67183
982 30 38.0 287 2 F81705
983 30 38.0 289 2 C87899
984 30 38.0 291 1 A31305
985 30 38.0 291 1 S18718
986 30 38.0 293 2 H70366
987 30 38.0 297 2 A72100
988 30 38.0 297 2 A86524
989 30 38.0 297 2 B95200
990 30 38.0 297 2 A98067
991 30 38.0 299 2 C35213
992 30 38.0 299 2 G64969
993 30 38.0 300 2 S76144
994 30 38.0 301 2 E72384
995 30 38.0 302 2 C49906
996 30 38.0 302 2 D81692
997 30 38.0 302 2 T24091
998 30 38.0 302 2 A69749
999 30 38.0 305 2 H86245
1000 30 38.0 306 2 H75358

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hypothetical prote
conserved hypothet
protein F16C3.2 [i
transcription fact
transcription fact
lysyl-tRNA synthet
4-hydroxybenzoate
benzoate octapheny
ABC transporter, A
hypothetical prote
rfbc protein - Shi
dUDP-4-dehydroram
hypothetical prote
ABC transporter, A
rfbc homolog - Xan
conserved hypothet
hypothetical prote
bifunctional nucle
LAO/AO transport s

ALIGNMENTS

RESULT 1
S28261
centromere protein E - human
N/Alternate names: centromere 312K protein; kinesin-related protein CENP-E
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C/Accession: S28261
R/Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.
Nature 359, 536-539, 1992
A/Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.
A/Reference number: S28261, MUID:93024922; PMID:1406971
A/Accession: S28261
A/Molecule type: mRNA
A/Residues: 1-2663 <YEN>
A/Cross-references: UNIPROT:Q02224; UNIPARC:UPI00001274FC; EMBL:Z15005; NID:g29864; PIDN
C/Genetics:
A/Gene: GDB:CENPE
A/Cross-references: GDB:361164; OMIM:117143
A/Map position: 4q24-4q25
C/Superfamily: centromere protein E; kinesin motor domain homology
C/Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop
F/7-335/Domain: kinesin motor domain homology <KMT>
F/86-93/Region: nucleotide-binding motif A (P-loop)
F/486-2183/Domain: coiled coil #status predicted <COI>
F/92/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 79; DB 1; Length 2663;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 189 RHYGETKMNQSSRS 203

RESULT 2
T14156
kinesin-related protein - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14156
R/Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.
Cell 91, 357-366, 1997
A/Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosom
A/Reference number: T17893; MUID:96028574; PMID:9363944
A/Accession: T14156

979 30 38.0 284 2 T23636
980 30 38.0 285 2 C64750
981 30 38.0 286 2 S67183
982 30 38.0 287 2 F81705
983 30 38.0 289 2 C87899
984 30 38.0 291 1 A31305
985 30 38.0 291 1 S18718
986 30 38.0 293 2 H70366
987 30 38.0 297 2 A72100
988 30 38.0 297 2 A86524
989 30 38.0 297 2 B95200
990 30 38.0 297 2 A98067
991 30 38.0 299 2 C35213
992 30 38.0 299 2 G64969
993 30 38.0 300 2 S76144
994 30 38.0 301 2 E72384
995 30 38.0 302 2 C49906
996 30 38.0 302 2 D81692
997 30 38.0 302 2 T24091
998 30 38.0 302 2 A69749
999 30 38.0 305 2 H86245
1000 30 38.0 306 2 H75358

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probable transcrip
hypothetical prote
conserved hypothet
protein F16C3.2 [i
transcription fact
transcription fact
lysyl-tRNA synthet
4-hydroxybenzoate
benzoate octapheny
ABC transporter, A
hypothetical prote
rfbc protein - Shi
dUDP-4-dehydroram
hypothetical prote
ABC transporter, A
rfbc homolog - Xan
conserved hypothet
hypothetical prote
bifunctional nucle
LAO/AO transport s

ALIGNMENTS

RESULT 1
S28261
centromere protein E - human
N/Alternate names: centromere 312K protein; kinesin-related protein CENP-E
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C/Accession: S28261
R/Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.
Nature 359, 536-539, 1992
A/Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.
A/Reference number: S28261, MUID:93024922; PMID:1406971
A/Accession: S28261
A/Molecule type: mRNA
A/Residues: 1-2663 <YEN>
A/Cross-references: UNIPROT:Q02224; UNIPARC:UPI00001274FC; EMBL:Z15005; NID:g29864; PIDN
C/Genetics:
A/Gene: GDB:CENPE
A/Cross-references: GDB:361164; OMIM:117143
A/Map position: 4q24-4q25
C/Superfamily: centromere protein E; kinesin motor domain homology
C/Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop
F/7-335/Domain: kinesin motor domain homology <KMT>
F/86-93/Region: nucleotide-binding motif A (P-loop)
F/486-2183/Domain: coiled coil #status predicted <COI>
F/92/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 79; DB 1; Length 2663;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 189 RHYGETKMNQSSRS 203

RESULT 2
T14156
kinesin-related protein - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14156
R/Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.
Cell 91, 357-366, 1997
A/Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosom
A/Reference number: T17893; MUID:96028574; PMID:9363944
A/Accession: T14156

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2954 <WOO>
A/Cross-references: UNIPROT:O42263; UNIPARC:UPI00000FDD80; EMBL:AF027728; NID:g2586070;
C/Genetics:
A/Gene: XCENP-E
C/Superfamily: centromere protein E; kinesin motor domain homology

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.00074;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 187 RHYGETKMNQSSRS 201

RESULT 3
T52425
kinesin-like protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52425
R/Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.
Gene 239, 309-316, 1999
A/Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic reg
A/Reference number: Z25171
A/Accession: T52425
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-823 <KAT>
A/Cross-references: UNIPROT:Q9S7P3; UNIPARC:UPI000009F1FC; EMBL:AB028468; PIDN:BAA88112.
C/Genetics:
A/Gene: ZCF125

Query Match 73.4%; Score 58; DB 2; Length 823;
Best Local Similarity 73.3%; Pred. No. 0.021;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
DB 184 RHYGETKMNQSSRS 198

RESULT 4
D96619
protein T30E16.9 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D96619
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: D96619
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-888 <STO>
A/Cross-references: UNIPROT:Q9LQ62; UNIPARC:UPI00000A1D8E; GB:AE005173; NID:g8778739; PI
C/Genetics:
A/Gene: T30E16.9
A/Map position: 1

Query Match 73.4%; Score 58; DB 2; Length 888;
Best Local Similarity 73.3%; Pred. No. 0.023;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 215 RHFGTNNVHSSRS 229
 ||:|||||

RESULT 5
 A47334
 Lckin kinesin-related antigen - Leishmania chagasi (fragment)
 C:Species: Leishmania chagasi
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
 C:Accession: A47334
 R:Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Ghalib, H.W.; Badaro, R.; Reed, S.G.
 Proc. Natl. Acad. Sci. U.S.A. 90, 775-779, 1993
 A>Title: Molecular characterization of a kinesin-related antigen of Leishmania chagasi
 A:Reference number: A47334; MUID:93133867; PMID:8421715
 A:Accession: A47334
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-955 <BUR>
 A:Cross-references: UNIPROT:P46865; UNIPARC:UPI00012DE6D; GB:L07879; NID:G308884; PIDN:
 A:Experimental source: MHOM/BR/82/BA-2.C1
 A>Note: sequence extracted from NCBI backbone (NCBIN:122864, NCBIP:122865)
 C:Keywords: ATP; nucleotide binding; P-loop
 F:13-398/Domain: kinesin motor domain homology <KMOT>
 F:122-129/Region: nucleotide-binding motif A (P-loop)

Query Match 68.4%; Score 54; DB 2; Length 955;
 Best Local Similarity 73.3%; Pred. No. 0.13;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 241 RHTASTKNDRSSRS 255
 ||:|||||

RESULT 6
 F84599
 probable kinesin heavy chain [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: F84599
 R:Lin, X.; Kaul, S.; Rounleay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.;
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: F84599
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-581 <STO>
 A:Cross-references: UNIPROT:Q9SUJ7; UNIPARC:UPI00009D929; GB:AE002093; NID:G4567365; PI
 A:Gene: At2g21300
 A:Map position: 2

Query Match 64.6%; Score 51; DB 2; Length 581;
 Best Local Similarity 66.7%; Pred. No. 0.28;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 205 RKIGETSLNRSRS 219
 ||:|||||

RESULT 7
 T06055
 hypothetical protein F19H22.50 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06055
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15184
 A:Accession: T06055
 A:Molecule type: DNA
 A:Residues: 1-834 <BEV>
 A:Cross-references: UNIPROT:Q9SVJ8; UNIPARC:UPI00009EC9D; EMBL:AL035679; GSPDB:GN00062;
 A:Experimental source: cultivar Columbia; BAC clone F19H22
 C:Genetics:
 A:Gene: ATSP:F19H22.50
 A:Map position: 4
 A:Introns: 63/1; 93/1; 126/3; 164/3; 196/2; 234/3; 276/2; 389/3; 422/3; 633/3; 726/2
 C:Superfamily: kinesin heavy chain; kinesin motor domain homology
 F:14-339/Domain: kinesin motor domain homology <KMOT>

Query Match 64.6%; Score 51; DB 2; Length 834;
 Best Local Similarity 66.7%; Pred. No. 0.41;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 214 RKIGETSLNRSRS 228
 ||:|||||

RESULT 8
 T30196
 kinesin motor protein 1 - smut fungus (Ustilago maydis)
 C:Species: Ustilago maydis (corn smut)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30196
 R:Lehmle, C.; Steinberg, G.; Snetelaar, K.M.; Schliwa, M.; Kahmann, R.; Bolker, M.
 EMBO J. 16, 3464-3473, 1997
 A>Title: Identification of a motor protein required for filamentous growth in Ustilago m
 A:Reference number: Z20770; MUID:97361828; PMID:9218789
 A:Accession: T30196
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1459 <LEH>
 A:Cross-references: UNIPROT:P87198; UNIPARC:UPI000006C405; EMBL:U92844; NID:G2062749; PI
 C:Genetics:
 A:Gene: kin1
 C:Function:
 A>Description: required for filamentous growth in Ustilago maydis

Query Match 63.3%; Score 50; DB 2; Length 1459;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 ||:|||||
 Db 487 RHVGATDWNRSRS 501
 ||:|||||

RESULT 9
 E86183
 hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: E86183
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E86183
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-198 <STO>

A;Cross-references: UNIPROT:Q9MAU7; UNIPARC:UPI00000A5EF7; GB:AE005172; NID:g7211991; P; C;Genetics: A;Map position: 1

Query Match 62.0%; Score 49; DB 2; Length 198;
Best Local Similarity 72.7%; Pred. No. 0.22;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKMNQR 11
||| |||:
Db 73 RHYNETRINQR 83

RESULT 10
S62328
kinesin-like DNA binding protein KID - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C;Accession: S62328
R;Tokai, N.; Fujimoto-Nishiyama, A.; Toyoshima, Y.; Yonemura, S.; Tsukita, S.; Inoue, J.
EMBO J. 15; 457-467, 1996
A;Title: Kid, a novel kinesin-like DNA binding protein, is localized to chromosomes and
A;Reference number: S62328; MUID:96174806; PMID:8599929
A;Accession: S62328
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-665 <TOK>
A;Cross-references: UNIPARC:UPI000017A356
C;Keywords: ATP; nucleotide binding; P-loop
F;44-374/Domain: kinesin motor domain homology <KMOT>
F;128-135/Region: nucleotide-binding motif A (P-loop)

Query Match 62.0%; Score 49; DB 2; Length 665;
Best Local Similarity 66.7%; Pred. No. 0.75;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRSSRS 15
||| |||:
Db 232 RTVGATRLNQRSSRS 246

RESULT 11
T06733
kinesin homolog F28P10.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06733
R;Quetier, F.; Choisein, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigian
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15793
A;Accession: T06733
A;Molecule type: DNA
A;Residues: 1-1070 <QUE>
A;Cross-references: UNIPROT:Q9SV36; UNIPARC:UPI00001775C8; EMBL:AL049655; GSPDB:GN000061
A;Experimental source: Cultivar Columbia; BAC clone F28P10
C;Genetics:
A;Gene: ATSP:F28P10.150
A;Map position: 3
A;Introns: 113/2; 153/3; 194/3; 256/3; 330/3; 377/1; 427/1; 456/3; 527/3; 572/3; 632/3;
C;Superfamily: kinesin-related protein KLP61F; kinesin motor domain homology
F;124-466/Domain: kinesin motor domain homology <KMOT>

Query Match 60.8%; Score 48; DB 2; Length 1070;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRSSRS 15
||| |||:
Db 311 RHAANTKMNTESSRS 325

RESULT 12
T29898

F:397-739/Domain: kinesin motor domain homology <KMOT>
F:481-488/Region: nucleotide-binding motif A (P-loop)

Query Match 59.5%; Score 47; DB 2; Length 754;
Best Local Similarity 60.0%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
| : : : : :
Db 598 RSVGKTQMEERLSRS 612
| : : : : :
| : : : : :

RESULT 15

S34830
kinesin-related protein ktaA - Arabidopsis thaliana
N:Alternate names: protein F7J7.210; protein T6K22.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 09-Dec-1993 #sequence revision 01-Dec-1995 #text_change 05-Oct-2004
C:Accession: S34830; T04958; T05170
R:Mitui, H.; Yamaguchi-Shinozaki, K.; Shinozaki, K.; Nishikawa, K.; Takahashi, H.
Mol. Gen. Genet. 238, 362-368, 1993
A:Title: Identification of a gene family (kat) encoding kinesin-like proteins in Arabidopsis
A:Reference number: S34830; MUID:93261419; PMID:8492804
A:Accession: S34830
A:Molecule type: mRNA
A:Residues: 1-793 <MIT>
A:Cross-references: UNIPROT:Q07970; UNIPARC:UPI000012DC4E; EMBL:D11371; NID:g303501; PID:R3evan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.P.X submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15391
A:Accession: T04958
A:Molecule type: DNA
A:Residues: 1-793 <BEV>
A:Cross-references: UNIPARC:UPI000012DC4E; EMBL:AL021960
A:Experimental source: cultivar Columbia; BAC clone F7J7
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Mew submitted to the Protein Sequence Database, August 1998
A:Reference number: Z15400
A:Accession: T05170
A:Molecule type: DNA
A:Residues: 1-397 <BEW>
A:Cross-references: UNIPARC:UPI0000000354; EMBL:AL031187
A:Experimental source: cultivar Columbia; BAC clone T6K22
C:Genetics:
A:Gene: ktaA
A:Map position: 4
A:Introns: 15/3; 89/3; 138/1; 174/3; 214/3; 282/3; 352/3; 377/3; 426/3; 473/1; 509/3; 568/3
A:Note: F7J7.210; T6K22.10
C:Keywords: ATP; nucleotide binding; P-loop
F:432-778/Domain: Kinesin motor domain homology <KMOT>
F:516-523/Region: nucleotide-binding motif A (P-loop)

Query Match 59.5%; Score 47; DB 2; Length 793;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
| : : : : :
Db 637 RSVGKTQMEERLSRS 651
| : : : : :
| : : : : :

RESULT 16
E85814
hypothetical protein Z3056 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85814
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85814

A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STO>
A:Cross-references: UNIPROT:Q8XB88; UNIPARC:UPI0000165823; GB:AE005174; NID:g12516072; F:481-488/Region: nucleotide-binding motif A (P-loop)
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3056
C:Superfamily: Escherichia coli probable membrane protein b1963

Query Match 58.2%; Score 46; DB 2; Length 102;
Best Local Similarity 69.2%; Pred. No. 0.4;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKNQRRSRS 15
| : : : : :
Db 24 YGSTKMEERLSRS 36
| : : : : :
| : : : : :

RESULT 17

E90966
hypothetical protein Ecs2701 [imported] - Escherichia coli (strain O157:H7, substrain R102)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E90966
R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Lehtii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H. DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a human enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90966
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAY>
A:Cross-references: UNIPROT:Q8XB88; UNIPARC:UPI00000D060B; GB:BA000007; PIDN:BA036124.1; F:481-488/Region: nucleotide-binding motif A (P-loop)
A:Experimental source: strain O157:H7, substrain R102
C:Genetics:
A:Gene: Ecs2701
C:Superfamily: Escherichia coli probable membrane protein b1963

Query Match 58.2%; Score 46; DB 2; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKNQRRSRS 15
| : : : : :
Db 30 YGSTKMEERLSRS 42
| : : : : :
| : : : : :

RESULT 18

G64960
probable membrane protein b1963 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: G64960
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64960
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-127 <BLAT>
A:Cross-references: UNIPARC:UPI00001680F0; GB:AE000288; GB:U00096; NID:g2367124; PIDN:AJ004001
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli probable membrane protein b1963
C:Keywords: transmembrane protein
F:93-109/Domain: transmembrane #status predicted <TW1>

Query Match 58.2%; Score 46; DB 2; Length 127;
Best Local Similarity 69.2%; Pred. No. 0.5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKMNQRSSRS 15
||| : |||
Db 30 YGSTWMEERLSRS 42
||| : |||
RESULT 19
T49235
kinesin-like protein - Arabidopsis thaliana
N:Alternate names: protein F7K15.60
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49235
R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25019
A:Accession: T49235
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-932 <OBE>
A:Cross-references: UNIPROT:Q9LXL3; UNIPARC:UPI0000052DA8; EMBL:AL353871; GSPDB:GN000061;
A:Experimental source: cultivar Columbia; BAC clone F7K15
C:Genetics:
A:Gene: ATSP:F7K15.60
A:Map position: 3
A:Introns: 76/1; 106/1; 139/3; 177/3; 205/1; 227/3; 247/3; 289/2; 355/3; 401/3; 430/3; 7
Query Match 58.2%; Score 46; DB 2; Length 932;
Best Local Similarity 60.0%; Pred. No. 3.8; Mismatches 4; Indels 0; Gaps 0;
Matches 9; Conservative 2;
QY 1 RHYGETKMNQRSSRS 15
||| : |||
Db 207 RQVGETALNDKSSRS 221
||| : |||
RESULT 20
C44259
kinesin heavy chain homolog KIF5 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C44259
R:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A:Title: Kinesin family in murine central nervous system.
A:Reference number: A44259; MUID:93077686; PMID:1447303
A:Accession: C44259
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-143 <AI2>
A:Cross-references: UNIPROT:P33175; UNIPARC:UPI00001775C7
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:118906)
C:Superfamily: kinesin motor domain; kinesin motor domain homology
F:1-143/Domain: kinesin motor domain homology (fragment) <KMO1>
Query Match 57.0%; Score 45; DB 2; Length 143;
Best Local Similarity 60.0%; Pred. No. 0.86;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 RHYGETKMNQRSSRS 15
||| : |||
Db 103 RHVAVTNMNEHSRS 117
||| : |||
RESULT 21
AF1393
glycosyl transferases homolog lmo2550 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1393
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <GLA>
A:Cross-references: UNIPROT:Q93RNO; UNIPARC:UPI0000054EBA; GB:NC_003210; PIDN:CAD00628.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2550
C:Superfamily: stress response protein csbb
Query Match 57.0%; Score 45; DB 2; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMNQRSS 12
||| : |||
Db 201 RHAGETKWNYS 212
||| : |||
RESULT 22
A11768
glycosyl transferases homolog lin2695 [imported] - Listeria innocua (strain Cliph11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A11768
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <GLA>
A:Cross-references: UNIPROT:Q927U3; UNIPARC:UPI000000CC955; GB:AL592022; PIDN:CAC97921.1;
A:Experimental source: strain Cliph11262
C:Genetics:
A:Gene: lin2695
C:Superfamily: stress response protein csbb
Query Match 57.0%; Score 45; DB 2; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETKMNQRSS 12
||| : |||
Db 201 RHAGETKWNYS 212
||| : |||
RESULT 23
C85065
kinesin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C85065
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488; PMID:10617198
A:Accession: C85065
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-777 <STO>
A:Cross-references: UNIPROT:Q9M0X6; UNIPARC:UPI000000A7F28; GB:NC_001268; NID:g7267279; P
C:Genetics:

A:Gene: AT4G05190
A:Map position: 4
C:Superfamily: kinesin-related protein KLP; kinesin motor domain homology

Query Match 57.0%; Score 45; DB 2; Length 777;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 621 RSVGKTHMNEQSSRS 635

RESULT 24
A41919
kinesin heavy chain - human
N:Contains: kinesin ATPase (EC 3.6.1.-)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A41919; S24603
R:Navone, F.; Niclas, J.; Hom-Bocher, N.; Sparks, L.; Bernstein, H.D.; McCaffrey, G.; Va
J. Cell Biol. 117, 1263-1275, 1992
A:Title: Cloning and expression of a human kinesin heavy chain gene: interaction of the
A:Reference number: A41919; MUID:92299683; PMID:1607388
A:Accession: A41919
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-963 <NAV>
A:Cross-references: UNIPROT:P33176; UNIPARC:UPI000012DE68; GB:X65873; NID:g34082; PIDN:C
C:Genetics:
A:Gene: GDB:KNS1; KNS
A:Cross-references: GDB:13532
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; nucleotide
F:9-331/Domain: kinesin motor domain homology <KMOT>
F:85-92/Region: nucleotide-binding motif A (P-loop)
F:402-860/Domain: rod #status predicted <RDD>
F:861-963/Domain: globular #status predicted <GBD>
F:91/Binding site: ATP (Lys) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 963;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 190 RHVAVTNMNEHSSRS 204

RESULT 25
A35075
kinesin heavy chain - longfin squid
N:Contains: kinesin ATPase (EC 3.6.1.-)
C:Species: Loligo pealeii (longfin squid)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A35075
R:Kosik, K.S.; Orecchio, L.D.; Schnapp, B.; Inouye, H.; Neve, R.L.
J. Biol. Chem. 265, 3278-3283, 1990
A:Title: The primary structure and analysis of the squid kinesin heavy chain.
A:Reference number: A35075; MUID:90153980; PMID:2137456
A:Accession: A35075
A:Molecule type: mRNA
A:Residues: 1-967 <KOS>
A:Cross-references: UNIPROT:P21613; UNIPARC:UPI000012DE69; GB:J05258; NID:g460682; PIDN:
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; methylated amino acid; microtub
F:9-332/Domain: kinesin motor domain homology <KMOT>
F:85-92/Region: nucleotide-binding motif A (P-loop)
F:392-861/Domain: rod #status predicted <RDD>
F:862-967/Domain: globular #status predicted <GBD>
F:27-174, 206/Binding site: phosphate (Ser) (covalent) #status predicted
F:32/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:91/Binding site: ATP (Lys) #status predicted

F:546/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 967;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:|:|:|
DB 190 RHVAVTNMNEHSSRS 204

RESULT 26
A31497
kinesin heavy chain - fruit fly (Drosophila melanogaster)
N:Contains: kinesin ATPase (EC 3.6.1.-)
C:Species: Drosophila melanogaster
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A31497
R:Yang, J.T.; Laymon, R.A.; Goldstein, L.S.B.
Cell 56, 879-889, 1989
A:Title: A three-domain structure of kinesin heavy chain revealed by DNA sequence and m
A:Reference number: A31497; MUID:89168428; PMID:2522352
A:Accession: A31497
A:Molecule type: mRNA
A:Residues: 1-975 <YAN>
A:Cross-references: UNIPROT:P17210; UNIPARC:UPI000011EE2A; GB:M24441; NID:gl57777; PIDN:
C:Genetics:
A:Gene: FlyBase:Khc
A:Cross-references: FlyBase:FBgn0001308
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; nucleotide
F:13-339/Domain: kinesin motor domain homology <KMOT>
F:92-99/Region: nucleotide-binding motif A (P-loop)
F:399-883/Domain: rod #status predicted <RDD>
F:884-975/Domain: globular #status predicted <GBD>
F:98/Binding site: ATP (Lys) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 975;
Best Local Similarity 60.0%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:~|:|:|:|
DB 197 RHIAVTNNNEHSSRS 211

RESULT 27
S37711
kinesin heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S37711
R:Kato, K.
J. Neurosci. 2, 704-711, 1991
A:Title: A collection of cDNA clones with specific expression patterns in mouse brain.
A:Reference number: S37707
A:Accession: S37711
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1027 <KAT>
A:Cross-references: UNIPROT:P28738; UNIPARC:UPI000016CE7C; EMBL:X61435; NID:g52796; PIDN:
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:9-333/Domain: kinesin motor domain homology <KMOT>
F:86-93/Region: nucleotide-binding motif A (P-loop)

Query Match 57.0%; Score 45; DB 2; Length 1027;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
|||:|:~|:|:|:|

Db 191 RHVAVTNMNEHSRS 205

RESULT 28

A38713

kinesin heavy chain - sea urchin (Strongylocentrotus purpuratus)
 N1:Contains: kinesin ATPase (SC 3.6.1.-)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
 C:Accession: A38713; S24308
 R:Wright, B.D.; Henson, J.H.; Wedaman, K.P.; Willy, P.J.; Morand, J.N.; Scholey, J.M.
 J. Cell Biol. 113, 817-833, 1991
 A:Title: Subcellular localization and sequence of sea urchin kinesin heavy chain: evidence
 A:Reference number: A38713; MUID:91225077; PMID:1827446
 A:Accession: A38713
 A:Molecule type: mRNA
 A:Residues: 1-1031 <WRI>
 A:Cross-references: UNIPROT:P35978; UNIPARC:UPI000012DE6B; GB:X56844; NID:gl0269; PIDN:C
 C:Superfamily: kinesin heavy chain; kinesin motor domain homology
 C:Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; mitosis; n
 F:9-331/Domain: kinesin motor domain homology <KMOT>
 F:84-91/Region: nucleotide-binding motif A (P-loop)
 F:393-857/Domain: rod #status predicted <RDS>
 F:858-1031/Domain: globular #status predicted <GSD>
 F:90/Binding site: ATP (Lys) #status predicted

Query Match 57.0%; Score 45; DB 1; Length 1031;
 Best Local Similarity 60.0%; Pred. No. 6.4;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
 || |||: ||||

Db 189 RHIAVTNMEHSRS 203

RESULT 29

I38510

neuronal kinesin heavy chain - human
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: I38510
 R:Niclas, J.; Navone, F.; Hon-Booher, N.; Vale, R.D.
 Neuron 12, 1059-1072, 1994
 A:Title: Cloning and localization of a conventional kinesin motor expressed exclusively
 A:Reference number: I38510; MUID:94242426; PMID:7514426
 A:Accession: I38510
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1032 <RES>
 A:Cross-references: UNIPROT:Q12840; UNIPARC:UPI000012DE6E; EMBL:U06698; NID:g497123; PID
 C:Superfamily: kinesin heavy chain; kinesin motor domain homology
 C:Keywords: nucleotide binding; P-loop
 F:10-333/Domain: kinesin motor domain homology <KMOT>
 F:86-93/Region: nucleotide-binding motif A (P-loop)

Query Match 57.0%; Score 45; DB 2; Length 1032;
 Best Local Similarity 60.0%; Pred. No. 6.4;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
 || |||: ||||

Db 191 RHVAVTNMNEHSRS 205

RESULT 30

S38983

kinesin-related protein 95K chain - sea urchin (Strongylocentrotus purpuratus) (fragment
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C>Date: 07-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 02-Feb-2001
 C:Accession: S38983; S72552
 R:Coile, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.
 Nature 366, 268-270, 1993
 A:Title: Novel heterotrimeric kinesin-related protein purified from sea urchin eggs.

A:Reference number: S38982; MUID:94050179; PMID:8232586
 A:Accession: S38983
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-294 <COL1>
 A:Cross-references: UNIPARC:UPI00001775CA; GB:U00996
 A:Accession: S72552
 A:Molecule type: protein
 A:Residues: 247-264 <COL2>
 A:Cross-references: UNIPARC:UPI00001775CB
 C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
 C:Keywords: nucleotide binding; P-loop
 F:1-279/Domain: kinesin motor domain homology (fragment) <KMOT>
 F:29-36/Region: nucleotide-binding motif A (P-loop)

Query Match 55.7%; Score 44; DB 2; Length 294;
 Best Local Similarity 60.0%; Pred. No. 2.7;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
 || |||: ||||

Db 134 RSVGSTNMNEHSRS 148

RESULT 31

C42640

kinesin-related protein KIP2 - Yeast (Saccharomyces cerevisiae)
 A:Alternate names: protein P2581; protein YPL155c
 C:Species: Saccharomyces cerevisiae
 C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
 C:Accession: C42640; S65166; S69444; S28232; S28234
 R:Roof, D.M.; Meluh, P.B.; Rose, M.D.
 J. Cell Biol. 118, 95-108, 1992
 A:Title: Kinesin-related proteins required for assembly of the mitotic spindle.
 A:Reference number: A42640; MUID:92317166; PMID:1618910
 A:Accession: C42640
 A:Molecule type: DNA
 A:Residues: 1-706 <ROO>
 A:Cross-references: UNIPROT:P28743; UNIPARC:UPI000012DE72; EMBL:Z11963; NID:g3852; PIDN:
 A:Note: sequence extracted from NCBI backbone (NCBIN:107719, NCBIP:107722)
 R:Purnelle, B.; Coster, F.; Goffeau, A.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S65154
 A:Accession: S65154
 A:Molecule type: DNA
 A:Residues: 1-706 <PUR>
 A:Cross-references: UNIPARC:UPI000012DE72; EMBL:Z73511; NID:gl370329; PIDN:CAA97860.1; P
 A:Experimental source: strain S288C (AB972)
 R:Purnelle, B.; Combiez, S.; Coster, F.; Naveau, F.; Goffeau, A.
 submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies
 que to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant
 A:Reference number: S69428
 A:Accession: S69444
 A:Molecule type: DNA
 A:Residues: 1-706 <PUW>
 A:Cross-references: UNIPARC:UPI000012DE72; EMBL:X96770; NID:gl403537; PIDN:CAA65566.1; P
 C:Genetics:
 A:Gene: SGD.KIP2; MIPS.YPL155c
 A:Cross-references: SGD.S0006076; MIPS.YPL155c
 A:Map position: 16L
 C:Superfamily: kinesin-related protein KIF2; kinesin motor domain homology
 C:Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
 F:159-499/Domain: kinesin motor domain homology #status atypical <KMOT>
 F:202-209/Region: nucleotide-binding motif A (P-loop)
 F:208/Binding site: ATP (Lys) #status predicted

Query Match 55.7%; Score 44; DB 1; Length 706;
 Best Local Similarity 66.7%; Pred. No. 6.6;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
 || |||: ||||

Db 330 RKIGETDYNARSSRS 344

RESULT 32

S58691

Kinesin-related protein KRP95 - sea urchin (Strongylocentrotus droebachiensis)

N:Alternate names: kinesin-2 chain B; KRP (85/95) 95K chain

C:Species: Strongylocentrotus droebachiensis

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S58691

J. Rashid, D.J.; Wedaman, K.P.; Scholey, J.M.

J. Mol. Biol. 252, 157-162, 1995

A:Title: Heterodimerization of the two motor subunits of the heterotrimeric kinesin, KRP

A:Reference number: S58691; MUID:95404610; PMID:7674298

A:Accession: S58691

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-742 <RAS>

A:Cross-references: UNIPROT:OTM453; UNIPARC:UPI0000173E01

C:Complex: heterotrimer of a 115K chain and two kinesin-related chains of 85K (PIR:S3898

C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology

C:Keywords: ATP; heterotrimer; microtubule binding; nucleotide binding; P-loop

F:9-345/Domain: kinesin motor domain homology <KMOT>

F:95-102/Region: nucleotide-binding motif A (P-loop)

F:101/Binding site: ATP (Lys) #status predicted

Query Match 55.7%; Score 44; DB 1; Length 742;

Best Local Similarity 60.0%; Pred. No. 7;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15

Db 200 RSVGSTNNNEHSSRS 214

RESULT 33

B56766

protein kinesin F2P9.27 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: B96766

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96766

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-987 <STO>

A:Cross-references: UNIPROT:Q9C9A8; UNIPARC:UPI00000A435A; GB:AE005173; NID:g7109485; PI

C:Genetics:

A:Gene: F2P9.27

A:Map position: 1

Query Match 55.7%; Score 44; DB 2; Length 987;

Best Local Similarity 60.0%; Pred. No. 9.3;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15

Db 698 RAVGSTALNERSRS 712

RESULT 34

T21134

hypothetical protein F20C5.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21134

R:Matthews, P.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z19381

A:Accession: T21134

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1130 <WIL>

A:Cross-references: UNIPROT:Q8MQ68; UNIPARC:UPI0000079539; EMBL:Z68161; PIDN:CAA92295.1;

A:Experimental source: clone F20C5

C:Genetics:

A:Gene: CESP:F20C5.2

A:Map position: 4

A:Introns: 15/3; 34/2; 69/2; 152/3; 183/3; 207/2; 314/3; 513/3; 546/2; 594/1; 632/3; 667

Query Match 55.7%; Score 44; DB 2; Length 1130;

Best Local Similarity 60.0%; Pred. No. 11;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15

Db 204 RSVGRTNNNEHSSRS 218

RESULT 35

C48835

kinesin-like protein (clone XKlp3) Klp - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: C48835

R:Vernos, I.; Heasman, J.; Wylie, C.

Dev. Biol. 157, 232-239, 1993

A:Title: Multiple kinesin-like transcripts in Xenopus oocytes.

A:Reference number: A48835; MUID:93246065; PMID:8482413

A:Accession: C48835

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-332 <VER>

A:Cross-references: UNIPROT:Q93478; UNIPARC:UPI00001775C9

A:Experimental source: oocytes

A>Note: sequence extracted from NCBI backbone (NCBI:P130977)

C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology

C:Keywords: nucleotide binding; P-loop

F:1-332/Domain: kinesin motor domain homology (fragment) <KMOT>

F:87-94/Region: nucleotide-binding motif A (P-loop)

Query Match 54.4%; Score 43; DB 2; Length 332;

Best Local Similarity 60.0%; Pred. No. 4.7;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15

Db 192 RSVGATNNNEHSSRS 206

RESULT 36

B44259

kinesin-related protein KIF3A - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004

C:Accession: B44259; S27872

R:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.

J. Cell Biol. 119, 1287-1296, 1992

A:Title: Kinesin family in murine central nervous system.

A:Reference number: A44259; MUID:93077686; PMID:1447303

A:Accession: B44259

A:Molecule type: mRNA

A:Residues: 1-701 <AI2>

A:Cross-references: UNIPROT:P28741; UNIPARC:UPI0000028DDC; EMBL:D12645; NID:g220469; PID

A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBI:P118911)

C;Complex: heterodimer with KIF3B (PIR:AS7107); the KIF3A/3B heterodimer associates with C;Function:

A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal tra C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide F;1-368/Domain: head globular #status predicted <HGL> F;15-351/Domain: kinesin motor domain homology <KMOT> F;100-107/Region: nucleotide-binding motif A (p-loop) F;369-599/Domain: helical rod #status predicted <ROD> F;600-701/Domain: tail globular #status predicted <TGL> F;106/Binding site: ATP (Lys) #status predicted

Query Match 54.4%; Score 43; DB 1; Length 701;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 206 RSVGATNNHSSRS 220

RESULT 37

AS7107

kinesin-related protein KIF3B - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: AS7107

R;Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.

J. Cell Biol. 130, 1387-1399, 1995

A;Title: KIF3A/3B: a heterodimeric kinesin superfamily protein that works as a microtubul

A;Reference number: AS7107; MUID:96032268; PMID:7559760

A;Accession: AS7107

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-747 <YAM>

A;Cross-references: UNIPROT:Q61771; UNIPARC:UPI000028ED1; GB:D26077; NID:G1060922; PIDN

A;Experimental source: brain

C;Complex: heterodimer with KIF3A (PIR:B44259); the KIF3A/3B heterodimer associates with C;Function:

A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal tra C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide F;1-363/Domain: head globular #status predicted <HGL> F;10-346/Domain: kinesin motor domain homology <KMOT> F;96-103/Region: nucleotide-binding motif A (p-loop) F;364-592/Domain: helical rod #status predicted <ROD> F;594-747/Domain: tail globular #status predicted <TGL> F;102/Binding site: ATP (Lys) #status predicted

Query Match 54.4%; Score 43; DB 1; Length 747;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 201 RSVGATNNHSSRS 215

RESULT 38

AS3939

kinesin homolog KHP1 - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-Dec-2004

C;Accession: AS3939

R;Walther, Z.; Vashishtha, M.; Hall, J.L.

J. Cell Biol. 126, 175-188, 1994

A;Title: The Chlamydomonas FLA10 gene encodes a novel kinesin-homologous protein.

A;Reference number: AS3939; MUID:94299638; PMID:8027176

A;Accession: AS3939

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-786 <WAL>

A;Cross-references: UNIPROT:Q46869; UNIPARC:UPI000012A838; EMBL:L33697; NID:G497696; PID

A;Note: authors translated the codon AAC for residue 753 as Asp

C;Genetics:

A;Gene: FLA10

C;Keywords: ATP; coiled coil; nucleotide binding; P-loop

F;11-359/Domain: kinesin motor domain homology <KMOT> F;97-104/Region: nucleotide-binding motif A (P-loop)

Query Match 54.4%; Score 43; DB 2; Length 786;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 203 RQVGATLMNQDSRS 217

RESULT 39

T45746

hypothetical protein F24M12.190 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T45746

R;Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999

A;Reference number: Z23012

A;Accession: T45746

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-968 <VT>

A;Cross-references: UNIPROT:Q9SD31; UNIPARC:UPI00000AB745; EMBL:AL132980

A;Experimental source: cultivar Columbia; BAC clone F24M12

C;Genetics:

A;Map position: 3

A;Introns: 69/1; 99/1; 132/3; 170/3; 198/1; 220/3; 242/3; 284/2; 396/3; 441/3; 514/1; 81

A;Note: F24M12.190

Query Match 54.4%; Score 43; DB 2; Length 968;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSSRS 15
DB 200 RQIGETALNEVSSRS 214

RESULT 40

C96661

kinesin-like protein, 73641-79546 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: C96661

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: C96661

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1056 <SPO>

A;Cross-references: UNIPROT:Q9CAC9; UNIPARC:UPI00000A6962; GB:AE005173; NID:G6456171; PI1

C;Genetics:

A;Gene: F24D7.17

A;Map position: 1

Query Match 54.4%; Score 43; DB 2; Length 1056;
Best Local Similarity 60.0%; Pred. No. 15;

Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | |
Db 650 RTVGATALNRSRS 664

RESULT 41

T13465
hypothetical protein T19F6.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13465
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Meyer, A.; et al. 1999. The Arabidopsis genome. Nature 391: 752-760.
A:Reference number: T13465
A:Accession: T13465
A:Molecule type: DNA
A:Residues: 1-1263 <BEV>
A:Cross-references: UNIPROT:Q9SU42; UNIPARC:UPI000008A4C5; EMBL:AL109619; GSPDB:GN000062;
A:Experimental source: cultivar Columbia; BAC clone T19F6
C:Genetics:
A:Gene: ATSP:T19F6.160
A:Map position: 4
A:Introns: 53/1; 83/1; 116/3; 156/3; 184/1; 206/3; 269/2; 269/2; 973/2; 1007/2; 1076/2; 1092/3;

Query Match 54.4%; Score 43; DB 2; Length 1263;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | |
Db 186 RKIGTSLNEISRS 200

RESULT 42

S38982
kinesin-related protein KRP85 - sea urchin (Strongylocentrotus purpuratus)
N:Alternate names: kinesin-2 chain A; KRP (85/95) 85K chain
C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S38982; S72551
R:Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.; Scholey, J.M.
Nature 366, 268-270, 1993
A:Title: Novel heterotrimeric kinesin-related protein purified from sea urchin eggs.
A:Reference number: S38982; MUID:94050179; PMID:8232586
A:Accession: S38982
A:Molecule type: mRNA
A:Residues: 1-699 <COL1>
A:Cross-references: UNIPROT:P46872; UNIPARC:UPI000012DE48; EMBL:L16993; NID:g295245; PID
A:Accession: S72551
A:Molecule type: protein
A:Residues: 2-5, 'X', 7-11, 59-64; 125-132; 222-226, 'X', 228-230 <COL2>
A:Cross-references: UNIPARC:UPI0000173DFF; UNIPARC:UPI0000173DFF; UNIPARC:UPI0000173DFF; UNIPARC:UPI0000173DFF;
C:Complex: heterotrimer of a 115K chain and two kinesin-related chains of 95K (PIR:S5869)
C:Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C:Keywords: ATP; heterotrimer; microtubule binding; nucleotide binding; P-loop
F:11-348/Domain: kinesin motor domain homology <RMOT>
F:97-104/Region: nucleotide-binding motif A (P-loop)
F:103/Binding site: ATP (Lys) #status predicted

Query Match 53.2%; Score 42; DB 1; Length 699;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | |
Db 203 RSVGATNMNRSRS 217

RESULT 43

T00434
probable kinesin heavy chain [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T30B22.20
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00434; A84916
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mao
submitted to the EMBL Data Library, October 1998
A:Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.
A:Reference number: Z14149
A:Accession: T00434
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-861 <ROU>
A:Cross-references: UNIPROT:Q22260; UNIPARC:UPI000009DA9E; EMBL:AC002535; NID:g2529657;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84916
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-861 <STO>
A:Cross-references: UNIPARC:UPI000009DA9E; GB:AE002093; NID:g2529677; PIDN:AAC62860.1; C
C:Genetics:
A:Gene: At2g47500; T30B22.20
A:Map position: 2
A:Introns: 44/1; 99/3; 147/3; 224/3; 248/3; 271/3; 299/1; 389/1; 424/3; 471/3; 523/2; 60
F:333-646/Domain: kinesin motor domain homology <KMOT>

Query Match 53.2%; Score 42; DB 2; Length 861;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | |
Db 507 RAVGSTALNDRSRS 521

RESULT 44

F72691
probable fumarate reductase flavoprotein subunit APE0950 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Dec-2004
C:Accession: F72691
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: F72691
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <KAW>
A:Cross-references: UNIPROT:Q9YDG3; UNIPARC:UPI000005DD5B; DDBJ:AP000060; NID:gs104188;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0950
C:Superfamily: succinate dehydrogenase, flavoprotein subunit (SDHA/APRA/LASPO); 3-oxo

Query Match 51.9%; Score 41; DB 2; Length 573;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RHYGETKNQR 11
| | | | |
Db 307 RHLGEKINER 317

RESULT 45

A44337
kinesin-related protein KLPA - Emericella nidulans

N:Alternate names: kinesin-like protein, KAR3-related, KLPA protein
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A44337; S24830
R:O'Connell, M.J.; Meluh, P.B.; Rose, M.D.; Morris, N.R.
J. Cell Biol. 120, 153-162, 1993
A:Title: Suppression of the bimC4 mitotic spindle defect by deletion of klpA, a gene encoding a kinesin-like protein
A:Reference number: A44337; MUID:93107178; PMID:8416986
A:Accession: A44337
A:Molecule type: mRNA
A:Residues: 1-770 <OLC>
A:Cross-references: UNIPROT:P28739; UNIPARC:UPI000012DEF6; GB:X64603; NID:g2703; PIDN:CA44337
A:Note: sequence extracted from NCBI backbone (NCBIP:121121)
C:Genetics:
A:Gene: KlpA
A:Map position: 1
C:Superfamily: kinesin-related protein KLPA; kinesin motor domain homology
C:Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
F:422-762/Domain: kinesin motor domain homology <XMOT>
F:514-521/Region: nucleotide-binding motif A (P-loop)
F:520/Binding site: ATP (Lys) #status predicted

Query Match 51.9%; Score 41; DB 1; Length 770;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 619 RSVATKANERSRS 633
|||:|||||

RESULT 46
T38749
kinesin-like protein 1 - fission yeast (Schizosaccharomyces pombe)
N:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38749; T48658; T11636
R:Olliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z21809
A:Accession: T38749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-832 <OLI>
A:Cross-references: UNIPROT:Q92376; UNIPARC:UPI000012DEF0; EMBL:Z99296; PIDN:CAB16597.1;
R:Pidoux, A.L.; Ledizet, M.; Cande, W.Z.
Mol. Biol. Cell 7, 1639-1655, 1996
A:Title: Fission yeast is a kinesin-related protein involved in mitotic spindle function
A:Reference number: Z24510; MUID:97053988; PMID:8898367
A:Accession: T48658
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-342, 'D', 344-832 <PID>
A:Cross-references: UNIPARC:UPI00001691C6; EMBL:U63916; PIDN:AAB88235.1
A:Experimental source: strain 972h(-)
R:Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z17303
A:Accession: T11636
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 761-832 <BAR>
A:Cross-references: UNIPARC:UPI000169036; EMBL:Z99260; NID:e1061997; PID:e349380
C:Genetics:
A:Gene: SPDB:SPAC3H5.03c
A:Map position: 1
A:Introns: 4/3; 216/1; 778/3
A:Note: SPAC3A11.14c
A:Note: intron positions not resolved (incomplete sequence)
C:Function:
A:Description: pkl1 shows microtubule-stimulated ATPase activity, nucleotide-sensitive B

C:Superfamily: kinesin-related protein KLPA; kinesin motor domain homology
C:Keywords: hydrolase; microtubule binding

Query Match 51.9%; Score 41; DB 2; Length 832;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 680 RFIAATKANERSRS 694
|||:|||||

RESULT 47
T03792
kinesin-related protein tck1 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03792
R:Wang, W.; Takezawa, D.; Narasimulu, S.B.; Reddy, A.S.N.; Poovaiah, B.W.
Plant Mol. Biol. 31, 87-100, 1996
A:Title: A novel kinesin-like protein with a calmodulin-binding domain.
A:Reference number: Z15089; MUID:96309387; PMID:8704162
A:Accession: T03792
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1265 <WAN>
A:Cross-references: UNIPROT:O24147; UNIPARC:UPI00000AD012; EMBL:U52078; NID:g1491930; PI
A:Experimental source: cultivar Petit Havana SR-1; tissue-type authors
C:Genetics:
A:Gene: tck1
F:890-1221/Domain: kinesin motor domain homology <XMOT>

Query Match 51.9%; Score 41; DB 2; Length 1265;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 1075 RHTTGTLNQEQRSS 1089
|||:|||||

RESULT 48
T07397
kinesin heavy chain-like protein (clone PKCBP) - potato
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07397
R:Reddy, A.S.; Narasimulu, S.B.; Safadi, F.; Golovkin, M.
Plant J. 10, 9-21, 1996
A:Title: A plant kinesin heavy chain-like protein is a calmodulin-binding protein.
A:Reference number: Z16008; MUID:96314858; PMID:8758976
A:Accession: T07397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1265 <RED>
A:Cross-references: UNIPROT:Q41460; UNIPARC:UPI00000AA86C; EMBL:L46702; NID:g1369851; PI
C:Keywords: GTP binding; microtubule binding
F:890-1216/Domain: kinesin motor domain homology <XMOT>

Query Match 51.9%; Score 41; DB 2; Length 1265;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSSRS 15
Db 1075 RHTTGTLNQEQRSS 1089
|||:|||||

RESULT 49
D85058
hypochemical protein AT4g04630 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: D85058
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: D85058
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-202 <STO>
 A:Cross-references: UNIPROT:Q9XEB6; UNIPARC:UPI00000A86FC; GB:NC_001268; NID:g7267221; E
 C:Genetics:
 A:Gene: AT4G04630
 A:Map position: 4

Query Match 50.6%; Score 40; DB 2; Length 202;
 Best Local Similarity 53.6%; Pred. NO. 10;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGETKMNQRSS 13
 ||:| |:
 DB 91 YGDSKSNRRSS 101

RESULT 50

A75088
 hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: A75088
 R:Anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75088
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <RAW>
 A:Cross-references: UNIPROT:Q9UZQ0; UNIPARC:UPI00000633B1; GB:AJ248286; GB:AL096836; NID
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1640

Query Match 50.6%; Score 40; DB 2; Length 219;
 Best Local Similarity 53.8%; Pred. NO. 11;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRSS 13
 :||| |:
 DB 12 KHYGETVLIENS 24

Search completed: April 21, 2006, 13:42:31
 Job time : 54 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:34:25 ; Search time 230 Seconds

(without alignment)

46.013 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKMQRSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	2585	Q4LE75 HUMAN	Q4LE75 homo sapien
2	79	100.0	2663	CENPE_HUMAN	Q02224 homo sapien
3	75	94.9	1558	Q4SEM9 TETNG	Q4SEM9 tetraodon n
4	71	89.9	160	Q35059 MOUSE	Q35059 mus musculus
5	71	89.9	549	Q7TPX4 MOUSE	Q7TPX4 mus musculus
6	71	89.9	2474	Q6RT24 MOUSE	Q6RT24 mus musculus
7	69	87.3	2954	Q42263 XENLA	Q42263 xenopus lae
8	58	73.4	807	Q94HV9 ARATH	Q94HV9 arabidopsis
9	58	73.4	823	Q9S7P3 ARATH	Q9S7P3 arabidopsis
10	58	73.4	888	Q9LQ62 ARATH	Q9LQ62 arabidopsis
11	54	68.4	842	Q7Q5F1 ANOGA	Q7Q5F1 anopheles g
12	54	68.4	859	Q61WZ2 LEIDO	Q61WZ2 leishmania
13	54	68.4	890	Q61WZ1 LEIDO	Q61WZ1 leishmania
14	54	68.4	955	KINL_LEICH	P46865 leishmania
15	54	68.4	1803	Q57UD0 9TRYP	Q57UD0 trypanosoma
16	53	67.1	578	Q57V46 9TRYP	Q57V46 trypanosoma
17	53	67.1	591	Q57V47 9TRYP	Q57V47 trypanosoma
18	53	67.1	1229	Q4QFM3 LEIMA	Q4QFM3 leishmania
19	53	67.1	2013	Q9VKI0 DROME	Q9VKI0 drosophila
20	53	67.1	2244	Q9NCG0 DROME	Q9NCG0 drosophila
21	53	67.1	2765	Q4QFM4 LEIMA	Q4QFM4 leishmania
22	53	67.1	2976	Q4QFM2 LEIMA	Q4QFM2 leishmania
23	52	65.8	168	Q54722 RAT	Q54722 rattus norv
24	52	65.8	459	Q9S830 ARATH	Q9S830 arabidopsis
25	52	65.8	810	Q57XT2 9TRYP	Q57XT2 trypanosoma
26	52	65.8	865	Q9SILL1 MACFA	Q9SILL1 macaca fasc
27	52	65.8	1266	Q7PCK6 MACFA	Q7PCK6 macaca fasc
28	52	65.8	1304	Q86VH0 HUMAN	Q86VH0 homo sapien
29	52	65.8	1335	Q86VH1 HUMAN	Q86VH1 homo sapien
30	52	65.8	1394	Q7M6Z5 RAT	Q7M6Z5 rattus norv
31	52	65.8	1394	Q7M6Z4 MOUSE	Q7M6Z4 mus musculus

32	65.8	1401	2	Q86VH2 HUMAN	Q86VH2 homo sapien
33	65.8	1931	2	Q9NCF9 DROME	Q9NCF9 drosophila
34	65.8	1931	2	Q9VKH9 DROME	Q9VKH9 drosophila
35	51	581	2	Q9SVU7 ARATH	Q9SVU7 arabidopsis
36	51	64.6	834	Q9SVJ8 ARATH	Q9SVJ8 arabidopsis
37	50	63.3	777	Q9VRK9 DROME	Q9VRK9 drosophila
38	50	63.3	746	Q57Za9 9TRYP	Q57Za9 trypanosoma
39	50	63.3	1043	Q4P5T9 USTMA	Q4P5T9 ustilago ma
40	50	63.3	1459	Q4PG67 USTMA	Q4PG67 ustilago ma
41	50	63.3	1459	P87198 USTMA	P87198 ustilago ma
42	50	63.3	1624	Q9U679 STRPU	Q9U679 strongyloce
43	49	62.0	146	Q91113 MORSA	Q91113 morone saxa
44	49	62.0	148	Q35232 MOUSE	Q35232 mus musculus
45	49	62.0	156	Q15719 DICDI	Q15719 dictyosteli
46	49	62.0	193	Q84JL8 ARATH	Q84JL8 arabidopsis
47	49	62.0	198	Q9MAU7 ARATH	Q9MAU7 arabidopsis
48	49	62.0	573	Q4SIJ2 TETNG	Q4SIJ2 tetraodon n
49	49	62.0	597	Q5R9A3 PONPY	Q5R9A3 pongo pygma
50	49	62.0	600	Q4R838 MACFA	Q4R838 macaca fasc
51	49	62.0	660	Q99LC7 MOUSE	Q99LC7 mus musculus
52	49	62.0	665	K1P22_HUMAN	K1P22_HUMAN
53	49	62.0	665	Q31F58 HUMAN	Q31F58 homo sapien
54	49	62.0	665	Q5REP4 PONPY	Q5REP4 pongo pygma
55	49	62.0	1363	Q58G59 BRARE	Q58G59 brachydanio
56	49	62.0	1885	Q869B8 DICDI	Q869B8 dictyosteli
57	49	62.0	1922	Q5ANP8 DICDI	Q5ANP8 dictyosteli
58	48	60.8	170	Q9AVD7 TOBAC	Q9AVD7 nicotiana t
59	48	60.8	406	Q4SKM2 TETNG	Q4SKM2 tetraodon n
60	48	60.8	657	Q510E8 RAT	Q510E8 rattus norv
61	48	60.8	862	Q851Z7 ORYSA	Q851Z7 oryza sativ
62	48	60.8	925	Q7VYJ8 CRYPV	Q7VYJ8 cryptospori
63	48	60.8	934	Q5CJ33 CRYHO	Q5CJ33 cryptospori
64	48	60.8	1034	Q4QDF2 LEIMA	Q4QDF2 leishmania
65	48	60.8	1061	Q4QDF3 LEIMA	Q4QDF3 leishmania
66	48	60.8	1062	Q4Q9P4 LEIMA	Q4Q9P4 leishmania
67	48	60.8	1070	Q9SV36 ARATH	Q9SV36 arabidopsis
68	48	60.8	1254	Q4QJC6 LEIMA	Q4QJC6 leishmania
69	48	60.8	2078	Q4Q3T1 LEIMA	Q4Q3T1 leishmania
70	47	59.5	347	Q93XF8 MAIZE	Q93XF8 zea mays (m
71	47	59.5	672	Q9GV93 CABEL	Q9GV93 caenorhabdi
72	47	59.5	686	Q61HG5 CABER	Q61HG5 caenorhabdi
73	47	59.5	699	QSM3_CABEL	QSM3_CABEL
74	47	59.5	754	ATK3_ARATH	P46875 arabidopsis
75	47	59.5	793	ATK1_ARATH	Q07970 arabidopsis
76	47	59.5	956	Q9GRN3 LEIMA	Q9GRN3 leishmania
77	47	59.5	990	Q8T135 DICDI	Q8T135 dictyosteli
78	46	58.2	102	Q8XB88 ECO57	Q8XB88 escherichia
79	46	58.2	108	Q7ACV4 ECO57	Q7ACV4 escherichia
80	46	58.2	121	YEDR_ECOLI	P76334 escherichia
81	46	58.2	127	Q8FGJ0 ECOL6	Q8FGJ0 escherichia
82	46	58.2	145	Q91115 MORSA	Q91115 morone saxa
83	46	58.2	465	Q8GW44 ARATH	Q8GW44 arabidopsis
84	46	58.2	469	Q8LEG9 ARATH	Q8LEG9 arabidopsis
85	46	58.2	818	Q7XN65 ORYSA	Q7XN65 oryza sativ
86	46	58.2	824	Q4SUU7 TETNG	Q4SUU7 tetraodon n
87	46	58.2	928	Q4REL2 TETNG	Q4REL2 tetraodon n
88	46	58.2	932	Q9LXL3 ARATH	Q9LXL3 arabidopsis
89	46	58.2	937	Q8LGU3 ARATH	Q8LGU3 arabidopsis
90	46	58.2	937	Q8L5J2 ARATH	Q8L5J2 arabidopsis
91	46	58.2	938	Q8LNZ2 ARATH	Q8LNZ2 arabidopsis
92	46	58.2	955	Q8S949 TOBAC	Q8S949 nicotiana t
93	46	58.2	958	Q969B4 GALA	Q969B4 giardia lam
94	46	58.2	1066	Q7QVT8 GALA	Q7QVT8 giardia lam
95	46	58.2	1107	Q3J2U3 9CHLO	Q3J2U3 stichococcu
96	46	58.2	1209	Q7Y1U0 GOSHI	Q7Y1U0 gosyplu h
97	45	57.0	145	Q91117 MORSA	Q91117 morone saxa
98	45	57.0	145	Q91114 MORSA	Q91114 morone saxa
99	45	57.0	145	Q91110 MORSA	Q91110 morone saxa
100	45	57.0	238	1 KIF5C RAT	P56536 rattus norv
101	45	57.0	315	Q927U3 LITIN	Q927U3 listeria in
102	45	57.0	315	Q91RNO LITSMO	Q91RNO listeria mo
103	45	57.0	317	Q9GMV1 MACFA	Q9GMV1 macaca fasc
104	45	57.0	345	Q6P164_HUMAN	Q6P164 homo sapien

105	45	57.0	346	2	Q5REP7_PONPY	Q5rep7	pongo pygma	178	44	55.7	782	2	Q9GV92_CABEL	Q9gv92	caenorhabdi
106	45	57.0	349	2	Q8CFE7_MOUSE	Q8cfe7	mus musculus	179	44	55.7	897	2	Q93XF3_MAIZE	Q93xf3	zea mays (m
107	45	57.0	349	2	Q504B9_BRARE	Q504b9	brachydanio	180	44	55.7	918	2	Q6F301_ORYZA	Q6f301	oryza sativ
108	45	57.0	351	2	Q6ETC4_HUMAN	Q6etc4	homo sapien	181	44	55.7	971	2	Q5JKW1_ORYZA	Q5jkw1	oryza sativ
109	45	57.0	351	2	Q66K46_HUMAN	Q66k46	homo sapien	182	44	55.7	987	2	Q9C9A8_ARATH	Q9c9a8	arabidopsis
110	45	57.0	351	2	Q6NS55_MOUSE	Q6ns55	mus musculus	183	44	55.7	1050	2	Q9C9S6_ARATH	Q9c9s6	arabidopsis
111	45	57.0	352	2	Q6PKD3_HUMAN	Q6pkd1	homo sapien	184	44	55.7	1130	2	Q8MQS8_CABEL	Q8mq8	caenorhabdi
112	45	57.0	354	2	Q93XF5_MAIZE	Q93xf5	zea mays (m	185	44	55.7	1172	2	Q7QSR2_GIALA	Q7qsr2	giardia lam
113	45	57.0	358	2	Q6NNT8_DROME	Q6nnt8	drosophila	186	44	55.7	1463	2	Q7XJW0_ORYZA	Q7xjw0	oryza sativ
114	45	57.0	394	2	Q7XALI_ORYZA	Q7xali	oryza sativ	187	44	55.7	2221	2	Q4QDF1_LEIMA	Q4qdf1	leishmania
115	45	57.0	590	2	Q6VL14_COTCO	Q6vl14	coturnix co	188	43	54.4	268	2	Q5W4S8_CHICK	Q5w4s8	gallus gall
116	45	57.0	642	2	Q7YLC8_ORYZA	Q7ylc8	oryza sativ	189	43	54.4	305	2	Q6PLD3_MOUSE	Q6pld3	mus musculus
117	45	57.0	745	1	ATK2_ARATH	P46864	arabidopsis	190	43	54.4	310	2	Q4SJV4_TETNG	Q4sjv4	tetraodon n
118	45	57.0	766	2	Q93XG3_MAIZE	Q93xg3	zea mays (m	191	43	54.4	408	2	Q8IWH8_HUMAN	Q8iwh8	homo sapien
119	45	57.0	777	2	Q9M0X6_ARATH	Q9m0x6	arabidopsis	192	43	54.4	408	2	Q8OUK1_MOUSE	Q8ouk1	mus musculus
120	45	57.0	790	2	Q6NQ77_ARATH	Q6nq77	arabidopsis	193	43	54.4	425	2	Q94JU6_ARATH	Q94ju6	arabidopsis
121	45	57.0	820	2	Q6GSA9_9TRYP	Q6gsa9	trypanosoma	194	43	54.4	443	2	Q8CGJ1_MOUSE	Q8cgj1	mus musculus
122	45	57.0	884	2	Q6H638_ORYZA	Q6h638	oryza sativ	195	43	54.4	447	2	Q6DCF1_YENLA	Q6dcf1	xenopus lae
123	45	57.0	916	2	Q4SNN2_TETNG	Q4snn2	tetraodon n	196	43	54.4	449	2	Q6DEG6_BRARE	Q6deg6	brachydanio
124	45	57.0	950	2	Q7PG43_ANOGA	Q7pg43	anopheles g	197	43	54.4	482	2	Q6IC70_CABBR	Q6ic70	caenorhabdi
125	45	57.0	956	1	KIF5C_MOUSE	P28738	mus musculus	198	43	54.4	569	2	Q4R4B6_MACFA	Q4r4b6	macaca fasc
126	45	57.0	956	2	Q6NX19_MOUSE	Q6nx19	mus musculus	199	43	54.4	698	2	Q5SX84_MOUSE	Q5sx84	mus musculus
127	45	57.0	957	1	KIF5C_HUMAN	P60282	homo sapien	200	43	54.4	699	2	Q98T11_XENLA	Q98t11	xenopus lae
128	45	57.0	963	1	KINH_HUMAN	P33176	homo sapien	201	43	54.4	701	1	KIF3A_MOUSE	P28741	mus musculus
129	45	57.0	963	1	KINH_MOUSE	P61768	mus musculus	202	43	54.4	701	2	Q7TSZ7_MOUSE	Q7tsz7	mus musculus
130	45	57.0	963	2	Q5VZ85_HUMAN	Q5vz85	homo sapien	203	43	54.4	702	1	KIF3A_HUMAN	Q9y496	homo sapien
131	45	57.0	963	2	Q5BL10_MOUSE	Q5bl10	mus musculus	204	43	54.4	702	2	Q5R4H3_PONPY	Q5r4h3	pongo pygma
132	45	57.0	967	1	KINH_LOLPE	P21613	loligo peal	205	43	54.4	702	2	Q4R628_MACFA	Q4r628	macaca fasc
133	45	57.0	975	1	KINH_DROME	P17210	drosophila	206	43	54.4	706	2	Q5F3C2_CHICK	Q5f3c2	gallus gall
134	45	57.0	986	2	Q6Z9D1_ORYZA	Q6z9d1	oryza sativ	207	43	54.4	728	2	Q4SJV3_TETNG	Q4sjv3	tetraodon n
135	45	57.0	987	2	Q8CHF7_MOUSE	Q8chf1	mus musculus	208	43	54.4	730	2	Q59EN1_HUMAN	Q59en1	homo sapien
136	45	57.0	998	2	Q6C348_YARLI	Q6c348	yarrowia li	209	43	54.4	739	2	Q5F423_CHICK	Q5f423	gallus gall
137	45	57.0	1003	2	Q6Z9D2_ORYZA	Q6z9d2	oryza sativ	210	43	54.4	744	2	Q93478_XENLA	Q93478	xenopus lae
138	45	57.0	1027	1	KINN_MOUSE	P33175	mus musculus	211	43	54.4	747	1	KIF3B_HUMAN	O15066	homo sapien
139	45	57.0	1027	2	Q6QLM7_RAT	Q6qlm7	rattus norv	212	43	54.4	747	1	KIF3B_MOUSE	Q61771	mus musculus
140	45	57.0	1027	2	Q6PDY7_MOUSE	Q6pyd7	mus musculus	213	43	54.4	747	2	Q8BNH4_MOUSE	Q8bnh4	mus musculus
141	45	57.0	1031	1	KINH_STRPU	P35978	strongyloce	214	43	54.4	757	2	Q8OU27_MOUSE	Q8ou27	mus musculus
142	45	57.0	1032	1	KINN_HUMAN	Q12840	homo sapien	215	43	54.4	765	2	Q93XG2_MAIZE	Q93xg2	zea mays (m
143	45	57.0	1032	2	Q5R9K7_PONPY	Q5r9k7	pongo pygma	216	43	54.4	767	2	Q22240_ARATH	Q22240	arabidopsis
144	45	57.0	1040	2	Q4S807_TETNG	Q4s807	tetraodon n	217	43	54.4	776	2	Q4T9W2_TETNG	Q4t9w2	tetraodon n
145	45	57.0	1043	2	Q4LE26_HUMAN	Q4le26	homo sapien	218	43	54.4	786	1	FLA10_CHLRE	P46869	chlamydomon
146	45	57.0	1060	2	Q4TBE0_TETNG	Q4tbe0	tetraodon n	219	43	54.4	810	2	Q7ZU82_BRARE	Q7zu82	brachydanio
147	45	57.0	1064	2	Q4S869_TETNG	Q4s869	tetraodon n	220	43	54.4	903	2	Q4XNS6_PLACH	Q4xns6	plasmodium
148	45	57.0	1105	2	Q5KE89_CRYNE	Q5ke89	cryptococcu	221	43	54.4	915	2	Q7FBI7_ORYZA	Q7fbi7	oryza sativ
149	45	57.0	1158	2	Q5DTP1_MOUSE	Q5dtp1	mus musculus	222	43	54.4	945	2	Q7X7H4_ORYZA	Q7x7h4	oryza sativ
150	45	57.0	1207	2	Q5SP68_CRYNE	Q5sp68	cryptococcu	223	43	54.4	954	2	Q9AMW8_ORYZA	Q9amw8	oryza sativ
151	45	57.0	1259	2	Q22326_ARATH	Q22326	arabidopsis	224	43	54.4	959	2	Q8S950_TOBAC	Q8s950	nicotiana t
152	45	57.0	1259	2	Q23102_ARATH	Q23102	arabidopsis	225	43	54.4	968	2	Q8SD31_ARATH	Q8sd31	arabidopsis
153	45	57.0	1260	2	Q9FHN8_ARATH	Q9fhn8	arabidopsis	226	43	54.4	974	2	Q8S905_ARATH	Q8s905	arabidopsis
154	45	57.0	1261	2	Q93130_ARATH	Q93130	arabidopsis	227	43	54.4	995	2	Q22974_ARATH	Q22974	arabidopsis
155	44	55.7	158	2	Q9FQL8_CYAPA	Q9fq18	cyanophora	228	43	54.4	1003	2	Q9LPQ5_ARATH	Q9lpq5	arabidopsis
156	44	55.7	264	2	Q696C0_GIALA	Q696c0	giardia lam	229	43	54.4	1037	2	Q9FH58_ARATH	Q9fh58	arabidopsis
157	44	55.7	325	2	Q5J2U2_CYAPA	Q5j2u2	cyanophora	230	43	54.4	1041	2	Q57XU6_9TRYP	Q57xu6	trypanosoma
158	44	55.7	328	2	Q93XG3_MAIZE	Q93xg1	zea mays (m	231	43	54.4	1056	2	Q9CAG9_ARATH	Q9cac9	arabidopsis
159	44	55.7	405	2	Q93XF2_MAIZE	Q93xf2	zea mays (m	232	43	54.4	1087	2	Q9F1G8_ARATH	Q9fig8	arabidopsis
160	44	55.7	438	2	Q5Z9S9_ORYZA	Q5z9s9	oryza sativ	233	43	54.4	1109	2	Q8W1Y3_ARATH	Q8w1y3	arabidopsis
161	44	55.7	447	2	Q6OKW3_CABBR	Q6okw3	caenorhabdi	234	43	54.4	1227	2	Q9SH47_ARATH	Q9sh47	arabidopsis
162	44	55.7	557	2	Q7PQZ7_ANOGA	Q7pqz7	anopheles g	235	43	54.4	1263	2	Q4QJD9_LEIMA	Q4qjd9	leishmania
163	44	55.7	561	2	Q7SUP8_IPOBA	Q7sup8	ipomoea bat	236	43	54.4	1263	2	Q9SU42_ARATH	Q9su42	arabidopsis
164	44	55.7	589	2	Q4FXG3_LEIMA	Q4fxg3	leishmania	237	43	54.4	1342	2	Q57YB0_9TRYP	Q57yb0	trypanosoma
165	44	55.7	590	2	Q4FXG4_LEIMA	Q4fxg4	leishmania	238	43	54.4	1661	2	Q4Z625_PLABE	Q4z625	plasmodium
166	44	55.7	607	2	Q9U5H3_CABEL	Q9u5h3	caenorhabdi	239	43	54.4	1673	2	Q560K9_CRYNE	Q560k9	cryptococcu
167	44	55.7	619	2	Q969C9_GIALA	Q969c9	giardia lam	240	43	54.4	1844	2	Q815U0_PLAF7	Q815u0	plasmodium
168	44	55.7	625	2	Q7QSW5_GIALA	Q7qsw5	giardia lam	241	43	54.4	1961	2	Q4QCT7_LEIMA	Q4qct7	leishmania
169	44	55.7	668	2	Q6CRW2_KJULA	Q6crw2	kluveromyc	242	43	54.4	2013	2	Q7RLW2_PLAYO	Q7rlw2	plasmodium
170	44	55.7	685	1	KIFZ_ASHGO	Q8j1g1	ashbya gosb	243	43	54.4	2756	2	Q9LJ60_ARATH	Q9lj60	arabidopsis
171	44	55.7	685	2	Q6S001_DICTDI	Q6s001	dictyosteli	244	42	53.2	150	2	Q9AVD6_TOBAC	Q9avd6	nicotiana t
172	44	55.7	706	1	KIF2_YEAST	P28743	saccharomyc	245	42	53.2	157	2	Q9AVD2_TOBAC	Q9avd2	nicotiana t
173	44	55.7	718	2	Q7R485_GIALA	Q7r485	giardia lam	246	42	53.2	168	2	Q35068_MOUSE	Q35068	mus musculus
174	44	55.7	735	2	Q9U0D5_TETTH	Q9u0d5	tetrahymena	247	42	53.2	185	2	Q5DAN3_SCHJA	Q5dan3	schistosoma
175	44	55.7	742	1	KRP95_STRPU	P46871	strongyloce	248	42	53.2	407	2	Q93XF9_MAIZE	Q93xf9	zea mays (m
176	44	55.7	742	2	Q7M453_STRDR	P46871	strongyloce	249	42	53.2	415	2	Q95U25_DROME	Q95u25	drosophila
177	44	55.7	782	2	Q19633_CABEL	Q19633	caenorhabdi	250	42	53.2	547	2	Q6Y252_ORYZA	Q6y252	oryza sativ

251	42	53.2	573	2	Q67L22_SYMTH	Q67L22 symbiobacte	324	40	50.6	168	2	Q8GWW1_ARATH	Q8GWW1 arabidopsia
252	42	53.2	631	2	Q6GPG0_XENLA	Q6GPG0 xenopus lae	325	40	50.6	168	2	Q8LF15_ARATH	Q8LF15 arabidopsia
253	42	53.2	638	2	Q58210_9TRYP	Q58210 trypanosoma	326	40	50.6	172	2	Q8AVD5_TORAC	Q8AVD5 nicotiana t
254	42	53.2	639	2	Q6P3R1_XENLA	Q6P3R1 xenopus tro	327	40	50.6	202	2	Q9XEB6_ARATH	Q9XEB6 arabidopsia
255	42	53.2	650	2	Q919A8_XENLA	Q919A8 xenopus lae	328	40	50.6	219	2	Q9UZQ0_PYRAB	Q9UZQ0 pyrococcus
256	42	53.2	651	2	Q918K0_XENLA	Q918K0 xenopus lae	329	40	50.6	248	2	Q4WMB9_ASPFU	Q4WMB9 aspergillus
257	42	53.2	651	2	Q91869_XENLA	Q91869 xenopus lae	330	40	50.6	302	2	Q8NLB0_CORGL	Q8NLB0 corynebacte
258	42	53.2	663	2	Q72YL5_XENLA	Q72YL5 xenopus lae	331	40	50.6	305	2	Q8M1H8_CORGL	Q8M1H8 corynebacte
259	42	53.2	681	2	Q5J2U4_PICAB	Q5J2U4 picea abies	332	40	50.6	332	2	Q7Q1P1_ARATH	Q7Q1P1 anopheles g
260	42	53.2	699	1	KRP85_PICAB	KRP852 strongyloce	333	40	50.6	353	2	Q503Q4_BRARE	Q503Q4 brachydanio
261	42	53.2	702	2	Q6FRP9_CANGA	Q6FRP9 candida gla	334	40	50.6	452	2	Q8C471_RAT	Q8C471 rattus norv
262	42	53.2	838	1	K1FC2_HUMAN	Q96AC6 homo sapien	335	40	50.6	480	2	Q8C901_MOUSE	Q8C901 mus musculu
263	42	53.2	861	2	Q22260_ARATH	Q22260 arabidopsia	336	40	50.6	481	2	Q8BNG3_MOUSE	Q8BNG3 mus musculu
264	42	53.2	889	2	Q703G7_EMENI	Q703G7 emericella	337	40	50.6	486	2	Q54720_RAT	Q54720 rattus norv
265	42	53.2	889	2	Q5ATU4_EMENI	Q5ATU4 aspergillus	338	40	50.6	535	2	Q17340_CABEL	Q17340 caenorhabdi
266	42	53.2	955	2	Q4WG42_ASPFU	Q4WG42 aspergillus	339	40	50.6	538	2	Q7PVB7_HUMAN	Q7PVB7 anopheles g
267	42	53.2	956	2	Q9C7B9_ARATH	Q9C7B9 arabidopsia	340	40	50.6	548	2	Q5T8B0_HOMO	Q5T8B0 homo sapien
268	42	53.2	983	2	Q84W97_ARATH	Q84W97 arabidopsia	341	40	50.6	578	2	Q87GW9_VIBPA	Q87GW9 vibrio para
269	42	53.2	997	2	Q8FG03_ARATH	Q8FG03 arabidopsia	342	40	50.6	581	2	Q8ZYMO_PYRAB	Q8ZYMO pyrobaculum
270	42	53.2	1003	2	Q7X932_VOLCA	Q7X932 volvox cart	343	40	50.6	629	2	Q51EX3_ENTHI	Q51EX3 entamoeba h
271	42	53.2	1009	2	Q7X931_CHLRE	Q7X931 chlamydomon	344	40	50.6	672	2	Q6FK03_CANGA	Q6FK03 candida gla
272	42	53.2	1033	2	Q91LH9_ARATH	Q91LH9 arabidopsia	345	40	50.6	721	2	Q7QDS6_ANOGA	Q7QDS6 anopheles g
273	42	53.2	1200	2	Q9FQL7_MAIZE	Q9FQL7 zea mays (m	346	40	50.6	773	1	Q6CC36_YARLI	Q6CC36 yarrowia li
274	42	53.2	1218	2	Q9V646_DROME	Q9V646 drosophila	347	40	50.6	784	2	KLP68_DROME	P46867 drosophila
275	42	53.2	1260	2	Q8VZV4_ARATH	Q8VZV4 arabidopsia	348	40	50.6	784	2	Q961H5_DROME	Q961H5 drosophila
276	42	53.2	1665	2	Q4FXV7_LEIMA	Q4FXV7 leishmania	349	40	50.6	814	1	CF102_HUMAN	Q82MV9 homo sapien
277	42	53.2	1801	2	Q5K8T9_CRYNE	Q5K8T9 cryptococcu	350	40	50.6	819	2	Q55HQ7_CRYNE	Q55HQ7 cryptococcu
278	42	53.2	1801	2	Q55LY0_CRYNE	Q55LY0 cryptococcu	351	40	50.6	819	2	Q5K793_CRYNE	Q5K793 cryptococcu
279	42	51.9	157	2	Q9AVD9_TORAC	Q9AVD9 nicotiana t	352	40	50.6	881	2	Q5ZKH9_CHICK	Q5ZKH9 gallus gall
280	41	51.9	204	2	Q5TV22_ANOGA	Q5TV22 anopheles g	353	40	50.6	897	2	Q60ZS0_CABBR	Q60ZS0 caenorhabdi
281	41	51.9	383	2	Q5XME5_CABEL	Q5XME5 caenorhabdi	354	40	50.6	897	2	Q88S42_ARATH	Q88S42 arabidopsia
282	41	51.9	458	2	Q5OR62_ENTHI	Q5OR62 entamoeba h	355	40	50.6	920	2	Q8A8X7_BACTN	Q8A8X7 bacteroides
283	41	51.9	573	2	Q9YDG3_AERPE	Q9YDG3 aeropyrum p	356	40	50.6	962	2	Q9FHD2_ARATH	Q9FHD2 arabidopsia
284	41	51.9	590	2	Q5FKC4_LACAC	Q5FKC4 lactobacilli	357	40	50.6	1042	2	Q55KA5_CRYNE	Q55KA5 cryptococcu
285	41	51.9	593	2	Q61B82_CABBR	Q61B82 caenorhabdi	358	40	50.6	1048	2	Q9NGN7_DROME	Q9NGN7 drosophila
286	41	51.9	605	2	Q4XPJ5_PLACH	Q4XPJ5 plasmodium	359	40	50.6	1048	2	Q9VKM4_DROME	Q9VKM4 drosophila
287	41	51.9	614	2	Q84VC0_ORYSA	Q84VC0 oryza sativ	360	40	50.6	1049	2	Q5K997_CRYNE	Q5K997 cryptococcu
288	41	51.9	635	2	Q759X8_ASHGO	Q759X8 ashbya gos	361	40	50.6	1051	2	Q94LW7_ARATH	Q94LW7 arabidopsia
289	41	51.9	697	2	Q70921_TETTH	Q70921 tetrahymena	362	40	50.6	1075	2	Q2SNE3_ARATH	Q2SNE3 arabidopsia
290	41	51.9	699	2	Q70AQ4_USTMA	Q70AQ4 ustilago ma	363	40	50.6	1142	1	G1N4_YEAST	Q12263 saccharomyc
291	41	51.9	763	2	Q5AZE0_EMENI	Q5AZE0 aspergillus	364	40	50.6	1149	2	Q4YBS0_PLABE	Q4YBS0 plasmodium
292	41	51.9	768	2	Q57WJ5_9TRYP	Q57WJ5 trypanosoma	365	40	50.6	1191	2	Q8GZU1_LYCES	Q8GZU1 lycopersico
293	41	51.9	769	2	Q4X092_ASPFU	Q4X092 aspergillus	366	40	50.6	1194	2	Q7R321_GIALA	Q7R321 giardia lam
294	41	51.9	770	1	KLPA_EMENI	P28739 emericella	367	40	50.6	1226	2	Q84VE4_ORYSA	Q84VE4 oryza sativ
295	41	51.9	787	2	Q57XZ5_9TRYP	Q57XZ5 trypanosoma	368	40	50.6	1248	2	Q7XPJ0_ORYSA	Q7XPJ0 oryza sativ
296	41	51.9	802	2	Q93928_NECHA	Q93928 nectria hae	369	40	50.6	1499	2	Q6S000_DICDI	Q6S000 dictyosteli
297	41	51.9	802	2	Q41L54_GIBZE	Q41L54 gibberella	370	40	50.6	1671	2	Q54M02_DICDI	Q54M02 dictyosteli
298	41	51.9	830	2	Q872F6_NEUCR	Q872F6 neuropora	371	40	50.6	2248	2	Q4P906_USTMA	Q4P906 ustilago ma
299	41	51.9	832	1	KLP1_SCHPO	Q92376 schizosacch	372	40	50.6	2743	2	Q4SR36_TETNG	Q4SR36 tetraodon n
300	41	51.9	833	2	Q5AW68_EMENI	Q5AW68 aspergillus	373	39.5	50.0	692	2	Q8C9Y7_MOUSE	Q8C9Y7 mus musculu
301	41	51.9	839	2	Q4QDJ5_LEIMA	Q4QDJ5 leishmania	374	39.5	50.0	738	1	ECT2_MOUSE	Q07139 mus musculu
302	41	51.9	857	2	Q93XF4_MAIZE	Q93XF4 zea mays (m	375	39.5	50.0	882	2	Q80VE4_MOUSE	Q80VE4 mus musculu
303	41	51.9	871	2	Q4RF96_TETNG	Q4RF96 tetraodon n	376	39.5	50.0	882	2	Q8CIH2_MOUSE	Q8CIH2 mus musculu
304	41	51.9	887	1	KI20A_MOUSE	P97329 mus musculu	377	39.5	50.0	882	2	Q8K2A0_MOUSE	Q8K2A0 mus musculu
305	41	51.9	887	2	Q542M4_MOUSE	Q542M4 mus musculu	378	39.5	50.0	913	2	Q8R3E2_MOUSE	Q8R3E2 mus musculu
306	41	51.9	924	2	Q86Z97_GIBMO	Q86Z97 gibberella	379	39.5	50.0	919	2	Q8DTR8_MOUSE	Q8DTR8 mus musculu
307	41	51.9	971	2	Q6YUL7_ORYSA	Q6YUL7 oryza sativ	380	39	49.4	33	2	Q7YV06_9TRYP	Q7YV06 trypanosoma
308	41	51.9	978	2	Q86ZC0_BOTCI	Q86ZC0 botrytis ci	381	39	49.4	144	2	Q512S0_ENTHI	Q512S0 entamoeba h
309	41	51.9	1012	2	Q528U1_MAGGR	Q528U1 magnaporthe	382	39	49.4	198	2	Q4PDX3_USTMA	Q4PDX3 ustilago ma
310	41	51.9	1032	2	Q9FIJ9_ARATH	Q9FIJ9 arabidopsia	383	39	49.4	216	2	Q80JY8_PICCO	Q80JY8 foot-and-no
311	41	51.9	1035	2	Q6YUL8_ARATH	Q6YUL8 oryza sativ	384	39	49.4	225	2	Q8HYX6_HUMAN	Q8HYX6 homo sapien
312	41	51.9	1035	2	Q8GS71_ARATH	Q8GS71 arabidopsia	385	39	49.4	291	2	Q4KPC9_CANFA	Q4KPC9 canis famli
313	41	51.9	1084	2	Q4P5V6_USTMA	Q4P5V6 ustilago ma	386	39	49.4	292	1	SHOX_HUMAN	O15266 homo sapien
314	41	51.9	1129	2	Q5W6L9_ORYSA	Q5W6L9 oryza sativ	387	39	49.4	292	2	Q5HYX7_HUMAN	Q5HYX7 homo sapien
315	41	51.9	1189	2	Q81825_DICDI	Q81825 dictyosteli	388	39	49.4	292	2	Q5IT45_HUMAN	Q5IT45 homo sapien
316	41	51.9	1193	2	Q6S005_DICDI	Q6S005 dictyosteli	389	39	49.4	340	2	Q9IAZ0_9PERC	Q9IAZ0 spherooides
317	41	51.9	1193	2	Q54UC9_DICDI	Q54UC9 dictyosteli	390	39	49.4	340	2	Q9IAZ6_9PERC	Q9IAZ6 spherooides
318	41	51.9	1257	2	Q4QBQ1_LEIMA	Q4QBQ1 leishmania	391	39	49.4	341	2	Q4RT97_TETNG	Q4RT97 tetraodon n
319	41	51.9	1265	2	Q24147_TORAC	Q24147 nicotiana t	392	39	49.4	365	2	Q6G474_BARHE	Q6G474 bartonella
320	41	51.9	1265	2	Q41460_SOLTU	Q41460 solanum tub	393	39	49.4	437	2	Q9Y013_PLAF7	Q9Y013 plasmodium
321	41	51.9	1335	2	Q9FME7_ARATH	Q9FME7 arabidopsia	394	39	49.4	444	2	Q6BY68_DEBHA	Q6BY68 debaryomyce
322	41	51.9	1394	2	Q582P0_9TRYP	Q582P0 trypanosoma	395	39	49.4	445	2	Q4LJ90_9BURK	Q4LJ90 burkholderi
323	40	50.6	165	2	Q35067_MOUSE	Q35067 mus musculu	396	39	49.4	447	1	ENGA_RALUS	Q8Y020 raietonia s

543	38	48.1	753	2	Q5X2A6_LEGPA	Q5x2a6	legionella	616	37	45.8	541	2	Q7VAL7_PROMA	Q7val7	prochloroco
544	38	48.1	753	2	Q5ZSU4_LEGPH	Q5zsu4	legionella	617	37	45.8	552	2	Q4QCZ0_LAIMA	Q4qcz0	leishmania
545	38	48.1	777	2	Q7QSE9_GIALA	Q7qse9	giardia lam	618	37	46.8	555	2	Q6RFT1_APIME	Q6rft1	apis mellif
546	38	48.1	803	2	Q583A3_9TRYP	Q583a3	trypanosoma	619	37	46.8	556	2	Q5C8T4_PETHY	Q5c8t4	petunia hyb
547	38	48.1	838	1	CEP1_CRYNE	Q5k9l1	cryptococcu	620	37	46.8	556	2	Q5IFI1_PETHY	Q5ifi1	petunia hyb
548	38	48.1	873	1	ZHX1_HUMAN	Q7u0y1	homo sapien	621	37	46.8	562	2	Q6C9W8_YARLI	Q6c9w8	yarowola li
549	38	48.1	873	1	ZHX1_MOUSE	P70121	mus musculus	622	37	46.8	574	2	Q960E9_DROME	Q960e9	drosoophila
550	38	48.1	873	1	ZHX1_RAT	Q8r515	rattus norv	623	37	46.8	574	2	Q8LGJ2_ARATH	Q8lgj2	arabidopsia
551	38	48.1	888	1	ETOL1_ARATH	Q9zqx6	arabidopsia	624	37	46.8	575	2	Q9LZM8_ARATH	Q9lzm8	arabidopsia
552	38	48.1	906	2	Q5DTL2_MOUSE	Q5dtl2	mus musculus	625	37	46.8	575	2	Q8HL17_ARATH	Q8hl17	arabidopsia
553	38	48.1	915	2	Q6GR48_XENLA	Q6gr48	xenopus lae	626	37	46.8	580	2	Q4RQ19_TETNG	Q4rq19	tetraodon n
554	38	48.1	916	2	Q6DEH6_BRARE	Q6deh6	brachydanio	627	37	46.8	580	2	Q5PLH3_SALPA	Q5plh3	salmomella
555	38	48.1	992	2	Q91XG0_MALZE	Q93xg0	zea mays (m	628	37	46.8	596	2	Q7CP97_SALTY	Q7cp97	salmomella
556	38	48.1	1006	2	K125_TOBAC	Q23826	nicotiana t	629	37	46.8	596	2	Q8FSL5_SALTI	Q8fsl5	salmomella
557	38	48.1	1032	2	Q80491_ARATH	Q80491	arabidopsia	630	37	46.8	601	1	FRDA_ECOLI	P00363	escherichia
558	38	48.1	1040	2	Q9A203_BACTN	Q8a203	bacteroides	631	37	46.8	602	2	Q83P37_SHIFL	Q83p37	shigella fl
559	38	48.1	1045	2	Q9AG20_DAUCA	Q9ag20	daucus caro	632	37	46.8	602	2	Q8FAL6_EGOLF	Q8fal6	escherichia
560	38	48.1	1056	2	Q5W7C6_ORYSA	Q5w7c6	oryza sativ	633	37	46.8	602	2	Q8XDO0_ECO57	Q8xd00	escherichia
561	38	48.1	1058	2	Q9SUU0_ARATH	Q9suu0	arabidopsia	634	37	46.8	603	2	Q889P6_ORYLA	Q889p6	oryzias lat
562	38	48.1	1058	2	Q9LZU5_ARATH	Q9lzu5	arabidopsia	635	37	46.8	603	2	Q8UUL1_ORYLA	Q8uul1	oryzias lat
563	38	48.1	1076	2	Q9SIB3_ARATH	Q9sib3	arabidopsia	636	37	46.8	624	2	Q57GN4_SALCH	Q57gn4	salmomella
564	38	48.1	1087	2	Q8G292_GIBMO	Q8g292	gibberella	637	37	46.8	628	2	Q585N4_9TRYP	Q585n4	trypanosoma
565	38	48.1	1248	2	Q6P9P4_BRARE	Q6p9p4	brachydanio	638	37	46.8	643	1	CTK2_XENLA	P79955	xenopus lae
566	38	48.1	1265	2	Q6RZ29_DICDI	Q6rzz9	dictyosteli	639	37	46.8	643	1	Q5XGK6_XENLA	Q5xgk6	xenopus lae
567	38	48.1	1300	1	ATG11_NEUCR	Q78055	neurospora	640	37	46.8	668	2	Q8CON1_MOUSE	Q8con1	mus musculus
568	38	48.1	1304	2	Q9SUK4_ARATH	Q9suk4	arabidopsia	641	37	46.8	675	2	Q5XGB8_XENTR	Q5xgb8	xenopus tro
569	38	48.1	1310	2	Q4RM26_TETNG	Q4rm26	tetraodon n	642	37	46.8	708	2	Q4SZU6_TETNG	Q4szu6	tetraodon n
570	38	48.1	1385	2	Q7TSP2_RAT	Q7tnp2	rattus norv	643	37	46.8	709	2	Q74ZE6_ASHGO	Q74ze6	ashya goss
571	38	48.1	1385	2	Q7TN17_RAT	Q7tn17	rattus norv	644	37	46.8	722	2	Q54IG2_DICDI	Q54ig2	dictyosteli
572	38	48.1	1386	2	Q984C1_RHILO	Q984c1	rhizobium l	645	37	46.8	727	2	Q54UT1_DICDI	Q54ut1	dictyosteli
573	38	48.1	1387	2	Q70MX5_MOUSE	Q70mx5	mus musculus	646	37	46.8	729	2	Q8HFA4_DROME	Q8hfa4	drosoophila
574	38	48.1	1387	2	Q6P9L6_MOUSE	Q6p9l6	mus musculus	647	37	46.8	729	2	Q9WU11_DROME	Q9wu11	drosoophila
575	38	48.1	1387	2	Q9NSR7_HUMAN	Q9nsr7	homo sapien	648	37	46.8	800	2	P92163_STRPU	P92163	strongyloce
576	38	48.1	1388	2	Q91785_XENLA	Q91785	xenopus lae	649	37	46.8	802	2	Q7RT59_PLAYO	Q7rt59	plasmaodiu
577	38	48.1	1793	2	Q4HXW9_GIBZE	Q4hwx9	gibberella	650	37	46.8	810	1	ZN33A_HUMAN	Q06730	homo sapien
578	38	48.1	1873	2	Q6S003_DICDI	Q6s003	dictyosteli	651	37	46.8	810	1	Q5VZ86_HUMAN	Q5vz86	homo sapien
579	38	48.1	1874	2	Q6LSQ4_CAEBR	Q6lsq4	caenorhabdi	652	37	46.8	839	2	Q94HCL_ORYSA	Q94hcl	oryza sativ
580	38	48.1	2121	2	Q4QC92_LEIMA	Q4qc92	leishmania	653	37	46.8	839	2	Q7XF10_ORYSA	Q7xf10	oryza sativ
581	37.5	47.5	465	2	Q4R302_MACFA	Q4r302	macaca fasc	654	37	46.8	841	2	Q5W6W1_ORYSA	Q5w6w1	oryza sativ
582	37	46.8	90	2	Q7JNH7_STRPU	Q7jnh7	strongyloce	655	37	46.8	844	2	Q6BT18_DBBHA	Q6bt18	debaromyce
583	37	46.8	153	2	Q9NFA2_PLAF7	Q9nfa2	plasmaodiu	656	37	46.8	859	2	Q8JDJ1_9HIV1	Q8jdj1	human immun
584	37	46.8	159	1	IGJ_MOUSE	P01592	mus musculus	657	37	46.8	862	2	Q6H535_ORYSA	Q6h535	oryza sativ
585	37	46.8	159	2	Q4QQV9_RAT	Q4qqv9	rattus norv	658	37	46.8	864	2	Q5KCB8_CRYNE	Q5kcb8	cryptococcu
586	37	46.8	167	2	Q9AVD3_TOBAC	Q9avd3	nicotiana t	659	37	46.8	865	2	Q6JWU2_9BACT	Q6jwu2	uncultured
587	37	46.8	178	2	Q89VY0_BRAJA	Q89vy0	bradyrhizob	660	37	46.8	872	2	Q9YZ97_9VIRU	Q9yz97	navel orang
588	37	46.8	176	2	Q59ZRB_CANAL	Q59zrb	candida alb	661	37	46.8	884	2	Q5U4X1_XENLA	Q5u4x1	xenopus lae
589	37	46.8	188	2	Q23604_CAEEL	Q23604	caenorhabdi	662	37	46.8	887	2	Q6DEA8_XENLA	Q6dea8	xenopus lae
590	37	46.8	190	2	Q6AH83_LEIXX	Q6ah83	leifsonia x	663	37	46.8	890	1	K120A_HUMAN	Q95235	homo sapien
591	37	46.8	226	2	Q59UUS_CANAL	Q59ju5	candida alb	664	37	46.8	890	2	Q8W5R6_ARATH	Q8w5r6	arabidopsia
592	37	46.8	233	2	Q4RE76_TETNG	Q4re76	tetraodon n	665	37	46.8	899	2	P74477_SYNY3	P74477	synchocyst
593	37	46.8	237	2	Q41PU7_GIBZE	Q41pu7	gibberella	666	37	46.8	909	2	Q9X103_ARATH	Q9x103	arabidopsia
594	37	46.8	253	2	Q632R6_BACCZ	Q632r6	bacillus ce	667	37	46.8	924	2	Q7ZWT5_XENLA	Q7zwt5	xenopus lae
595	37	46.8	255	2	Q8A6G0_BACTN	Q8a6g0	bacteroides	668	37	46.8	929	2	Q5VWA9_HUMAN	Q5vwa9	homo sapien
596	37	46.8	290	2	Q8TYK4_METKA	Q8tyk4	methanopyru	669	37	46.8	933	2	Q88F05_XENLA	Q88f05	xenopus lae
597	37	46.8	292	2	Q602L2_METCA	Q602l2	methylococc	670	37	46.8	938	2	Q7SDI4_NEUCR	Q7sdi4	neurospora
598	37	46.8	304	2	Q5AH08_CANAL	Q5ah08	candida alb	671	37	46.8	948	2	Q5XGE8_XENTR	Q5xge8	xenopus tro
599	37	46.8	308	2	Q612G6_CAEBR	Q612g6	caenorhabdi	672	37	46.8	960	2	Q23404_ARATH	Q23404	arabidopsia
600	37	46.8	329	1	Y135_MYCPN	P75263	mycoplasma	673	37	46.8	963	2	Q55JE1_CRYNE	Q55je1	cryptococcu
601	37	46.8	374	2	Q5F3M7_CHICK	Q5f3m7	gallus gall	674	37	46.8	1016	2	Q6QIY7_XENNE	Q6qiyl7	xenorhabdu
602	37	46.8	404	2	Q7PTN3_ANOGA	Q7ptn3	anopheles g	675	37	46.8	1018	2	Q5NNWC_GOSHI	Q5nnw6	gossypium h
603	37	46.8	404	2	Q5TXC8_ANOGA	Q5txc8	anopheles g	676	37	46.8	1027	2	Q8A549_BACTN	Q8a549	bacteroides
604	37	46.8	420	2	Q8SRB7_ENCCU	Q8srb7	encephalito	677	37	46.8	1028	2	Q6GSA8_HUMAN	Q6gsa8	homo sapien
605	37	46.8	445	2	Q5NA73_ORYSA	Q5na73	oryza sativ	678	37	46.8	1029	1	K1P17_HUMAN	Q9p2e2	homo sapien
606	37	46.8	449	1	Q6SDH7_BACLD	Q6sdh7	bacillus li	679	37	46.8	1029	2	Q53YS6_HUMAN	Q53ys6	homo sapien
607	37	46.8	465	1	L1F10_CANAL	Q9p4e5	candida alb	680	37	46.8	1055	2	Q8RWW4_ARATH	Q8rww4	arabidopsia
608	37	46.8	465	2	Q5APE3_CANAL	Q5ape3	candida alb	681	37	46.8	1055	2	Q8W5R5_ARATH	Q8w5r5	arabidopsia
609	37	46.8	469	2	Q6UNX5_NICBE	Q6unx5	nicotiana b	682	37	46.8	1056	1	K125_ARATH	P82266	arabidopsia
610	37	46.8	496	2	Q5L378_GEOKA	Q5l378	geobacillus	683	37	46.8	1068	2	Q9VNC7_DROME	Q9vnc7	drosoophila
611	37	46.8	507	2	Q52024_HALSA	Q52024	halobacteri	684	37	46.8	1116	2	Q5FAM3_BRAOL	Q5fam3	brassica ol
612	37	46.8	512	2	Q528B5_MAGGR	Q528b5	magnaporthe	685	37	46.8	1121	2	Q9SVI8_ARATH	Q9svi8	arabidopsia
613	37	46.8	513	2	Q6Z488_ORYSA	Q6z488	oryza sativ	686	37	46.8	1162	2	Q9LPQ7_ARATH	Q9lpq7	arabidopsia
614	37	46.8	538	2	Q59VZ1_CANAL	Q59vz1	candida alb	687	37	46.8	1188	2	Q9SE56_DROME	Q9se56	drosoophila
615	37	46.8	539	2	Q82FQ5_STRAW	Q82fq5	streptomyce	688	37	46.8	1195	2	Q9C7T0_ARATH	Q9c7t0	arabidopsia

689	37	46.8	1196	2	Q7RL15_PLAYO	Q7rl15 plasmodium	762	36	45.6	313	2	Q9ZR03_CICAR	Q9zru3 ciccr ariet
690	37	46.8	1212	2	Q4Q7F9_LEIMA	Q4q7f9 leishmania	763	36	45.6	322	2	Q4QKX1_HAB18	Q4qkx1 haemophilus
691	37	46.8	1215	2	Q7KTI7_DROME	Q7kti7 drosophila	764	36	45.6	323	1	MRAW_GLUOX	Q5fkx3 gluconobact
692	37	46.8	1274	1	ARMI_DROME	Q615k9 drosophila	765	36	45.6	326	2	Q6BGJ6_PARTE	Q6bgj6 paramesichia
693	37	46.8	1361	2	Q04264_ARATH	Q04264 arabidopsis	766	36	45.6	326	2	Q8FKS0_EC0L6	Q8fks0 escherichia
694	37	46.8	1437	2	Q5JNZ9_ORYSA	Q5jnz9 oryza sativ	767	36	45.6	330	1	RS2_MYCPU	Q98q36 mycoplasma
695	37	46.8	1461	2	Q8Y9F6_DROME	Q8y9f6 drosophila	768	36	45.6	333	2	Q4LJE1_9BURK	Q4ljel caenorhabdi
696	37	46.8	1463	2	Q9GYZ0_STRPU	Q9gyz0 strongyloce	769	36	45.6	344	2	Q61754_CABEL	Q61754 caenorhabdi
697	37	46.8	1474	2	Q8T4M0_DROME	Q8t4m0 drosophila	770	36	45.6	356	2	Q54JY7_DICTDI	Q54jy7 dictyosteli
698	37	46.8	1503	2	Q8T4L8_DROME	Q8t4l8 drosophila	771	36	45.6	359	2	Q51206_NEIME	Q51206 neisseria m
699	37	46.8	1503	2	Q7KTI8_DROME	Q7kti8 drosophila	772	36	45.6	373	2	Q6GND5_XENLA	Q6gnd5 xenopus lae
700	37	46.8	1506	2	Q4N7X6_THEPA	Q4n7x6 theileria p	773	36	45.6	374	2	Q6ZN11_HUMAN	Q6zn11 homo sapien
701	37	46.8	1509	2	Q9SP10_DROME	Q9sp10 drosophila	774	36	45.6	375	2	Q93066_BRANA	Q93066 brassica na
702	37	46.8	1509	2	Q5VLQ8_DROME	Q5vlg8 drosophila	775	36	45.6	384	1	HEPI_PEDHE	Q95819 pedobacter
703	37	46.8	1509	2	Q81PG1_DROME	Q81pg1 drosophila	776	36	45.6	385	2	Q7BQX3_9ENTR	Q7bqx3 serratia en
704	37	46.8	1605	2	Q17887_CABEL	Q17887 caenorhabdi	777	36	45.6	388	2	Q9X6U4_NEIME	Q9x6u4 neisseria m
705	37	46.8	1609	2	Q9GRC3_CABEL	Q9grc3 caenorhabdi	778	36	45.6	396	2	Q88UG5_LACPL	Q88ug5 lactobacill
706	37	46.8	1619	2	Q77382_PLAUF7	Q77382 plasmodium	779	36	45.6	401	2	Q9CBV4_MYCLE	Q9cbv4 mycobacteri
707	37	46.8	1641	2	Q5LJZ2_DROME	Q5ljz2 drosophila	780	36	45.6	408	2	Q9GHK2_3SOLA	Q9ghk2 lycium afri
708	37	46.8	1843	2	Q5JLC8_ORYSA	Q5jlc8 oryza sativ	781	36	45.6	411	1	MSK2_MEDSA	Q51138 medicago sa
709	37	46.8	2158	2	Q9LUT5_ARATH	Q9lut5 arabidopsis	782	36	45.6	421	2	Q9W5Q1_DROME	Q9w5q1 drosophila
710	37	46.8	2391	2	Q5D862_HUMAN	Q5d862 homo sapien	783	36	45.6	421	2	Q81NC2_BACAN	Q81nc2 bacillus an
711	37	46.8	2523	2	Q9VTP0_DROME	Q9vtp0 drosophila	784	36	45.6	422	2	Q6AIW9_DESPS	Q6aiw9 desulfotale
712	36	45.6	72	2	Q8Y0W3_RALSTONIA	Q8y0w3 ralstonia s	785	36	45.6	436	2	Q7S185_NEUCR	Q7s185 neurospora
713	36	45.6	77	2	Q82PE4_STRAW	Q82pe4 streptomyce	786	36	45.6	445	2	Q63US9_BURPS	Q63us9 burkholderi
714	36	45.6	82	2	Q5TSJ6_ANOGA	Q5tsj6 anopheles g	787	36	45.6	447	1	Y418_HATIN	Q41k84 gibberella
715	36	45.6	83	2	Q4TE09_TETNG	Q4te09 tetraodon n	788	36	45.6	453	2	Q4IK84_GIBZE	Q4ik84 gibberella
716	36	45.6	101	2	Q68775_YERPE	Q68775 yersinia pe	789	36	45.6	453	2	Q4HN01_CAMLA	Q4hn01 campylobact
717	36	45.6	101	2	Q74YJ1_YERPE	Q74yj1 yersinia pe	790	36	45.6	460	2	Q62JW8_BURMA	Q62jw8 burkholderi
718	36	45.6	101	2	Q935D1_SALT1	Q935d1 salmonella	791	36	45.6	468	2	Q5JN15_ORYSA	Q5jnl5 oryza sativ
719	36	45.6	139	2	Q51610_9ZZZZ	Q51610 plasmid col	792	36	45.6	479	2	Q7T318_BRARE	Q7t318 brachydanio
720	36	45.6	139	2	Q51625_9ZZZZ	Q51625 plasmid col	793	36	45.6	482	2	Q5J4W3_FUGRU	Q5j4w3 fugu rubrip
721	36	45.6	152	2	Q5J8X5_HUMAN	Q5j8x5 homo sapien	794	36	45.6	486	2	Q96700_3CAEN	Q96700 illyanassa o
722	36	45.6	159	2	Q35057_MOUSE	Q35057 mus musculu	795	36	45.6	494	2	Q4P3K0_USTWA	Q4p3k0 ustilago ma
723	36	45.6	160	2	Q35063_MOUSE	Q35063 mus musculu	796	36	45.6	494	2	Q5L7S9_BACFN	Q5l7s9 bacteroides
724	36	45.6	163	2	Q54719_RAT	Q54719 rattus norv	797	36	45.6	505	2	Q5V1P6_HALMA	Q5v1p6 halomarcula
725	36	45.6	166	2	Q8R7A3_TRETN	Q8r7a3 thermoanaer	798	36	45.6	512	2	Q9H6Q9_HUMAN	Q9h6q9 homo sapien
726	36	45.6	168	2	Q79N46_LACLC	Q79n46 lactococcus	799	36	45.6	513	2	Q47919_FISSU	Q47919 fischerella
727	36	45.6	174	2	Q4IMX3_GIBZE	Q4imx3 gibberella	800	36	45.6	512	2	Q8YKT1_ANASP	Q8ykt1 anabaena sp
728	36	45.6	174	2	Q717T1_MOUSE	Q717t1 mus musculu	801	36	45.6	515	2	Q4SEA0_TETNG	Q4sea0 tetraodon n
729	36	45.6	179	2	Q9MCV1_BPHK0	Q9mcv1 bacterioph	802	36	45.6	538	2	Q7UHD3_RHOBA	Q7uhd3 rhodopirall
730	36	45.6	182	1	LEP_BACCL	Q10cvt bacillus ca	803	36	45.6	555	2	Q8D625_VIBVU	Q8d625 vibrio vuln
731	36	45.6	182	2	Q5L265_GEOKA	Q5l265 geobacillus	804	36	45.6	564	2	Q54UR1_DICDI	Q54uri dictyosteli
732	36	45.6	197	2	Q7VGK9_HELHP	Q7vgk9 helicobacte	805	36	45.6	565	2	Q5KMD1_CRYNE	Q5kmd1 cryptococcu
733	36	45.6	198	1	SCPB_STRMU	Q7zak9 streptococc	806	36	45.6	566	2	Q7KZ68_HUMAN	Q7kz68 homo sapien
734	36	45.6	199	2	Q8UJ22_AGR75	Q8uju2 agrobacteri	807	36	45.6	571	2	Q7MD48_VIBVU	Q7md48 vibrio vuln
735	36	45.6	202	2	Q9XUW8_CABEL	Q9xuw8 caenorhabdi	808	36	45.6	582	2	Q5CKC7_CRYHO	Q5ckc7 cryptospori
736	36	45.6	203	2	Q5FWC3_MOUSE	Q5fwc3 mus musculu	809	36	45.6	583	2	Q5CR50_CRYPV	Q5cr50 cryptospori
737	36	45.6	204	2	Q927S3_LISIN	Q927s3 listeria in	810	36	45.6	583	2	Q9KLR7_VIBCH	Q9klr7 vibrio chol
738	36	45.6	204	2	Q71WK8_LISMF	Q71wk8 listeria mo	811	36	45.6	586	2	Q7Q4J4_ANOGA	Q7q4j4 anopheles g
739	36	45.6	204	2	Q8Y485_LISMO	Q8y485 listeria mo	812	36	45.6	587	2	Q6Z3Z9_ORYSA	Q6z3z9 oryza sativ
740	36	45.6	204	2	Q8ONN3_9PHYC	Q8onn3 ectocarpus	813	36	45.6	594	2	Q55XK3_CRYNE	Q55xk3 cryptococcu
741	36	45.6	214	2	Q48637_9LACT	Q48637 lactococcus	814	36	45.6	598	2	Q4V1B4_BACCZ	Q4v1b4 bacillus ce
742	36	45.6	229	2	Q6R023_CABEL	Q6r023 caenorhabdi	815	36	45.6	598	2	Q6D032_ERWCT	Q6d032 erwina car
743	36	45.6	232	2	Q5FBG4_9HYPO	Q5fbg4 fusarium sp	816	36	45.6	610	2	Q32582_EC0LI	Q32582 escherichia
744	36	45.6	238	2	Q5JN14_ORYSA	Q5jnl4 oryza sativ	817	36	45.6	613	2	Q93LNA_XANCV	Q93lna xanthomonas
745	36	45.6	246	2	Q30519_MYCSM	Q30519 mycobacteri	818	36	45.6	622	2	Q4V9Q4_BRARE	Q4v9q4 brachydanio
746	36	45.6	248	2	Q7D7I3_MYCTU	Q7d7i3 mycobacteri	819	36	45.6	622	2	Q60443_CRIGR	Q60443 cricetulus
747	36	45.6	248	2	Q7T214_MYCBO	Q7t214 mycobacteri	820	36	45.6	626	1	X159C_DROME	Q9xlu4 drosophila
748	36	45.6	248	2	Q33244_MYCTU	Q33244 mycobacteri	821	36	45.6	628	2	Q5SM09_CRYNE	Q5sm09 cryptococcu
749	36	45.6	255	2	Q9AKN6_RICMO	Q9akn6 rickettsia	822	36	45.6	628	2	Q5K8R0_CRYNE	Q5k8r0 cryptococcu
750	36	45.6	262	2	Q83YW9_MYCPA	Q83yw9 streptomyce	823	36	45.6	631	2	Q60SW1_CAEBR	Q60sw1 caenorhabdi
751	36	45.6	262	2	Q82GA8_STRAW	Q82ga8 streptomyce	824	36	45.6	666	2	Q4QR27_XENLA	Q4qr27 xenopus lae
752	36	45.6	262	2	Q82H10_STRAW	Q82h10 streptomyce	825	36	45.6	673	1	KIFC1_HUMAN	Q9bwl9 homo sapien
753	36	45.6	263	2	Q4HEA9_CAMCO	Q4hea9 campylobact	826	36	45.6	673	2	Q5SU09_HUMAN	Q5su09 homo sapien
754	36	45.6	265	2	Q49792_MYCLE	Q49792 mycobacteri	827	36	45.6	693	2	Q5X163_RAT	Q5x163 rattus norv
755	36	45.6	265	2	Q9S375_MYCLE	Q9s375 mycobacteri	828	36	45.6	695	2	Q9Z4I4_NEIME	Q9z4i4 neisseria m
756	36	45.6	269	2	Q6PC56_BRARE	Q6pc56 brachydanio	829	36	45.6	696	2	Q9H755_HUMAN	Q9h755 homo sapien
757	36	45.6	286	2	Q5L243_GEOKA	Q5l243 geobacillus	830	36	45.6	702	2	Q5AR20_WMENI	Q5arz0 aspergillus
758	36	45.6	299	2	Q63S97_BURPS	Q63s97 burkholderi	831	36	45.6	702	2	Q7YYK0_CRYPV	Q7yyk0 cryptospori
759	36	45.6	299	2	Q6ZLS8_BURMA	Q6zls8 burkholderi	832	36	45.6	709	2	Q6P4A5_HUMAN	Q6p4a5 homo sapien
760	36	45.6	300	1	MRAW_CHLTR	Q84274 chlamydia t	833	36	45.6	714	2	Q15718_DICDI	Q15718 dictyosteli
761	36	45.6	311	1	MRAW_PORGI	Q7nmn0 porphyromon	834	36	45.6	714	2	Q5CU31_CRYHO	Q5cuj31 cryptospori

835	36	45.6	715	2	Q9US53_SCHPO	Q9ue53 schizosacch	908	36	45.6	1743	2	Q9XWX5_CABEL	Q9xwx5 caenorhabdi
836	36	45.6	719	2	Q4KMP0_HUMAN	Q4kmp0 homo sapien	909	36	45.6	1748	2	Q61TP1_CAEBR	Q61tp1 caenorhabdi
837	36	45.6	720	2	Q6GMS7_HUMAN	Q6gms7 homo sapien	910	36	45.6	1749	1	X113A_MOUSE	Q9eqw7 mus musculu
838	36	45.6	730	2	Q86Z96_GIBMO	Q86z96 gibberella	911	36	45.6	1752	2	Q9H193_HUMAN	Q9h193 homo sapien
839	36	45.6	743	2	Q5R7M5_PONPY	Q5r7m5 pongo pygma	912	36	45.6	1757	2	Q9H194_HUMAN	Q9h194 homo sapien
840	36	45.6	753	2	Q09471_HUMAN	Q09471 homo sapien	913	36	45.6	1767	2	Q70AM4_RAT	Q70am4 rattus norv
841	36	45.6	762	2	Q7YV00_9TRYP	Q7yv00 trypanosoma	914	36	45.6	1768	2	Q5THQ2_HUMAN	Q5thq2 homo sapien
842	36	45.6	780	2	Q6P0K1_BRARE	Q6p0k1 brachydanio	915	36	45.6	1780	2	Q5T9M3_HUMAN	Q5t9m3 homo sapien
843	36	45.6	783	2	Q5U4W5_XENLA	Q5u4w5 xenopus lae	916	36	45.6	1780	2	Q9UFR5_HUMAN	Q9ufr5 homo sapien
844	36	45.6	789	2	Q61BQ0_CAEBR	Q61bq0 caenorhabdi	917	36	45.6	1798	2	Q4S8D9_TETNG	Q4s8d9 tetraodon n
845	36	45.6	789	2	Q9SP24_CABEL	Q9sp24 caenorhabdi	918	36	45.6	1803	1	Q5THQ3_HUMAN	Q5thq3 homo sapien
846	36	45.6	791	2	Q7112J1_RAT	Q7112j1 rattus norv	919	36	45.6	1805	1	X113A_HUMAN	Q9h1h9 homo sapien
847	36	45.6	792	1	K1FC2_MOUSE	O08672 mus musculu	920	36	45.6	1820	2	Q96Q89_HUMAN	Q96q89 homo sapien
848	36	45.6	792	2	Q9BPU3_DICDI	Q9bpu3 dictyosteli	921	36	45.6	1820	2	Q5T9N0_HUMAN	Q5t9n0 homo sapien
849	36	45.6	805	1	X110A_DROME	Q96020 drosophila	922	36	45.6	1826	1	X113B_HUMAN	Q9hqt8 homo sapien
850	36	45.6	808	2	Q5Z155_CHICK	Q5z155 gallus gall	923	36	45.6	1830	2	Q4P9C7_USTMA	Q4p9c7 ustilago ma
851	36	45.6	820	2	Q4SFK9_TETNG	Q4sfk9 tetraodon n	924	36	45.6	1867	2	Q4R101_TETNG	Q4r101 tetraodon n
852	36	45.6	829	1	SPD2_CAEBR	Q61dp2 caenorhabdi	925	36	45.6	1982	2	Q4SFX7_TETNG	Q4sfx7 tetraodon n
853	36	45.6	829	2	Q6FV25_CANGA	Q6fv25 candida gla	926	36	45.6	2262	2	Q4RF46_TETNG	Q4rf46 tetraodon n
854	36	45.6	840	2	Q4G6N4_LEIMA	Q4g6n4 leishmania	927	36	45.6	2335	2	Q6PM77_9PICO	Q6pmt7 foot-and-mo
855	36	45.6	859	2	Q9FW70_ORYSA	Q9fw70 oryza sativ	928	36	45.6	2335	2	Q9C2N9_9PICO	Q9c2n9 foot-and-mo
856	36	45.6	864	2	Q5QL86_ORYSA	Q5ql86 oryza sativ	929	36	45.6	2340	2	Q6PMU2_9PICO	Q6pmu2 foot-and-mo
857	36	45.6	867	2	Q7ZU15_BRARE	Q7zu15 brachydanio	930	35.5	44.9	107	2	Q4T0X3_TETNG	Q4t0x3 tetraodon n
858	36	45.6	867	2	Q9PUU5_BRARE	Q9puu5 brachydanio	931	35.5	44.9	294	2	Q8L619_ARATH	Q8l619 arabidopsis
859	36	45.6	871	2	Q5XGE1_XENTR	Q5xge1 xenopus tro	932	35.5	44.9	294	2	Q9SY11_ARATH	Q9sy11 arabidopsis
860	36	45.6	878	2	Q4SHJ9_TETNG	Q4shj9 tetraodon n	933	35.5	44.9	469	1	Y0B1_CABEL	Q02255 caenorhabdi
861	36	45.6	882	2	Q5CVF6_CRYPV	Q5cvf6 cryptospori	934	35.5	44.9	570	2	Q55XR3_CRYNE	Q55xr3 cryptococcu
862	36	45.6	882	2	Q5CHP4_CRYHO	Q5chp4 cryptospori	935	35.5	44.9	570	2	Q5KM77_CRYNE	Q5km77 cryptococcu
863	36	45.6	886	2	Q6W85_ORYSA	Q6w85 oryza sativ	936	35.5	44.9	574	2	Q9V4A1_DROME	Q9v4a1 drosophila
864	36	45.6	895	2	Q6LNA4_ARATH	Q6lna4 arabidopsis	937	35.5	44.9	649	2	Q6NNT2_DROME	Q6nnt2 drosophila
865	36	45.6	897	2	Q6DFB2_XENLA	Q6dfb2 xenopus lae	938	35.5	44.9	3004	2	Q4SN41_TETNG	Q4sn41 tetraodon n
866	36	45.6	904	2	Q6DBE5_ERWCT	Q6dbe5 erwinia car	939	35.5	44.9	3902	2	Q4SC60_TETNG	Q4sc60 tetraodon n
867	36	45.6	915	1	ATCU_VIBCH	Q6dbes erwinia car	940	35	44.3	58	2	Q8D124_WIGBR	Q8d124 wigglewort
868	36	45.6	919	2	Q4WG65_ASPPU	Q4wg65 aspergillus	941	35	44.3	72	2	Q860T2_CHICK	Q860t2 gallus gall
869	36	45.6	919	2	Q9FZ06_ARATH	Q9fz06 arabidopsis	942	35	44.3	86	2	Q502C6_BRARE	Q502c6 brachydanio
870	36	45.6	927	2	Q4U8G8_THEAN	Q4u8g8 theileria a	943	35	44.3	87	1	VP08_BEAPS	Q9f1u0 bacterioph
871	36	45.6	939	2	Q41P54_GIBZE	Q41p54 gibberella	944	35	44.3	88	2	Q7QUG7_GIALA	Q7qug7 giardia lam
872	36	45.6	941	2	Q4N163_THEPA	Q4n163 theileria p	945	35	44.3	88	2	Q5QN10_ORYSA	Q5qni0 oryza sativ
873	36	45.6	972	2	Q51UW9_MAGGR	Q51uw9 magnaporthe	946	35	44.3	92	1	DBH_BUCAI	P57144 buchnera ap
874	36	45.6	984	2	Q9U0K0_PLASF7	Q9u0k0 plasmodium	947	35	44.3	95	2	Q6Z6N7_ORYSA	Q6z6n7 oryza sativ
875	36	45.6	1004	2	Q4WJ17_ASPPU	Q4wj17 aspergillus	948	35	44.3	101	2	Q8V977_9VIRU	Q8v977 hop mosaic
876	36	45.6	1014	2	Q93RN9_XENNE	Q93rn9 xenorhabdus	949	35	44.3	102	2	Q5RHI7_BRARE	Q5rhi7 brachydanio
877	36	45.6	1025	2	Q5R8P8_PONPY	Q5r8p8 pongo pygma	950	35	44.3	102	2	Q5SNV3_BRARE	Q5snv3 brachydanio
878	36	45.6	1038	1	K1F17_MOUSE	Q99pw8 mus musculu	951	35	44.3	104	2	Q502B5_BRARE	Q502es brachydanio
879	36	45.6	1087	2	Q6SA74_9VIRU	Q6sa74 cherry chlo	952	35	44.3	121	2	Q9Z4H2_STRCO	Q9z4h2 streptomyce
880	36	45.6	1087	2	Q65A77_9VIRU	Q65a77 amasya cher	953	35	44.3	122	2	Q5I314_ECOLI	Q5i314 escherichia
881	36	45.6	1116	2	Q7Z5E0_HUMAN	Q7z5e0 homo sapien	954	35	44.3	124	2	Q9F3Z7_NEIME	Q9f3z7 neisseria m
882	36	45.6	1175	2	Q13632_HUMAN	Q13632 homo sapien	955	35	44.3	126	2	Q6GB05_STAAS	Q6gbq5 staphylococ
883	36	45.6	1184	2	Q7Y1L9_CRYPV	Q7y1l9 cryptospori	956	35	44.3	126	2	Q5H194_STAAC	Q5h194 staphylococ
884	36	45.6	1184	2	Q5CH49_CRYHO	Q5ch49 cryptospori	957	35	44.3	126	2	Q7A764_STAAN	Q7a764 staphylococ
885	36	45.6	1193	2	Q7X7H8_ORYSA	Q7x7h8 oryza sativ	958	35	44.3	126	2	Q8NXW7_STAAW	Q8nxw7 staphylococ
886	36	45.6	1206	2	Q9N7C1_HUMAN	Q9n7c1 homo sapien	959	35	44.3	126	2	Q9W29_9VIRU	Q9w29 staphylococ
887	36	45.6	1219	2	Q85W55_HUMAN	Q85w55 homo sapien	960	35	44.3	129	2	Q9PA02_XYLFA	Q9pa02 xyella faa
888	36	45.6	1236	2	Q54WQ2_DICDI	Q54wq2 dictyosteli	961	35	44.3	129	2	Q5MXB1_9CLOS	Q5mxb1 mint vein b
889	36	45.6	1264	2	Q5A444_CANAL	Q5a444 candida alb	962	35	44.3	130	2	Q6YMA9_LITLI	Q6yma9 littorina l
890	36	45.6	1264	2	Q5A496_CANAL	Q5a496 candida alb	963	35	44.3	131	2	Q6YAX2_METCA	Q6yax2 methylococ
891	36	45.6	1268	2	Q9LUG0_ARATH	Q9lugo arabidopsis	964	35	44.3	138	2	Q4TCF3_TETNG	Q4tcf3 tetraodon n
892	36	45.6	1289	2	Q4T042_TETNG	Q4t042 tetraodon n	965	35	44.3	147	2	Q58IT3_9ACTO	Q58it3 streptomyce
893	36	45.6	1292	2	Q9LDN0_ARATH	Q9ldn0 arabidopsis	966	35	44.3	150	2	Q95068_HUMAN	Q95068 homo sapien
894	36	45.6	1293	2	Q8H7Z2_ORYSA	Q8h7z2 oryza sativ	967	35	44.3	151	2	Q91116_MORSA	Q91116 morone saxa
895	36	45.6	1307	2	Q8GY37_ARATH	Q8gy37 arabidopsis	968	35	44.3	151	2	Q91112_MORSA	Q91112 morone saxa
896	36	45.6	1307	2	Q9S710_ARATH	Q9s710 arabidopsis	969	35	44.3	155	2	Q35230_MOUSE	Q35230 mus musculu
897	36	45.6	1313	2	Q8L7Y8_ARATH	Q8l7y8 arabidopsis	970	35	44.3	160	1	K1F1C_MOUSE	Q35071 mus musculu
898	36	45.6	1371	2	Q51XB4_MAGGR	Q51xb4 magnaporthe	971	35	44.3	162	2	Q9W3Y0_DROME	Q9w3y0 drosophila
899	36	45.6	1373	2	Q81WES_HUMAN	Q81we9 homo sapien	972	35	44.3	165	2	Q8FBY3_ECOLA	Q8fby3 escherichia
900	36	45.6	1396	1	ATG26_EMENT	Q5b4c9 emericeila	973	35	44.3	167	2	Q9AVD4_TOBAC	Q9avd4 nicotiana t
901	36	45.6	1427	2	Q14207_HUMAN	Q14207 homo sapien	974	35	44.3	168	1	DYR_LACLA	Q59487 lactococcu
902	36	45.6	1427	2	Q16580_HUMAN	Q16580 homo sapien	975	35	44.3	172	2	Q6VU59_CHICK	Q6vu59 gallus gall
903	36	45.6	1479	2	Q4RIU7_TETNG	Q4riu7 tetraodon n	976	35	44.3	172	2	Q6VU62_CHICK	Q6vu62 gallus gall
904	36	45.6	1493	2	Q7PXF9_ANGOA	Q7pxf9 anopheles g	977	35	44.3	172	2	Q861N2_CHICK	Q861n2 gallus gall
905	36	45.6	1556	2	Q5KNG1_CRYNE	Q5kng1 cryptococcu	978	35	44.3	175	2	Q6AZH4_XENLA	Q6azh4 xenopus lae
906	36	45.6	1556	2	Q55Z46_CRYNE	Q55z46 cryptococcu	979	35	44.3	179	2	Q6JGT4_CHICK	Q6jgt4 gallus gall
907	36	45.6	1662	2	O23274_ARATH	O23274 arabidopsis	980	35	44.3	179	2	Q6JGT8_CHICK	Q6jgt8 gallus gall

981 35 44.3 179 2 Q6JGU6 CHICK Q6JGU6 gallus gall
 982 35 44.3 179 2 Q6JGV1 CHICK Q6JGV1 gallus gall
 983 35 44.3 180 2 Q9GIT3 CHICK Q9GIT3 gallus gall
 984 35 44.3 180 2 Q9GIT5 CHICK Q9GIT5 gallus gall
 985 35 44.3 180 2 Q9GIT7 CHICK Q9GIT7 gallus gall
 986 35 44.3 181 2 Q4NBE1_9M1CC Q4NBE1 arthrobacte
 987 35 44.3 188 1 SCBP_LACLA Q5CG34 lactococcus
 988 35 44.3 193 2 Q5M1H9 STRT1 Q5M1H9 streptococc
 989 35 44.3 193 2 Q5M621_STRT2 Q5M621 paracloamyd
 990 35 44.3 207 2 Q6WAS5_PARUW Q6WAS5 schistosoma
 991 35 44.3 209 2 Q5D8V3_SCHJA Q5D8V3 schistosoma
 992 35 44.3 215 1 TRAJ9_ECOLI Q00738 escherichia
 993 35 44.3 222 1 FLPA_THEVO Q979P2 thermoplasma
 994 35 44.3 232 2 O15103 HUMAN O15103 homo sapien
 995 35 44.3 232 2 Q98231 CHICK Q98231 gallus gall
 996 35 44.3 232 2 Q7YPM6 CHICK Q7YPM6 gallus gall
 997 35 44.3 232 2 Q7YPM7 CHICK Q7YPM7 gallus gall
 998 35 44.3 235 2 Q87A11_XYLFT Q87A11 xyella fas
 999 35 44.3 239 2 Q5WCK1_BACSK Q5WCK1 bacillus cl
 1000 35 44.3 252 2 Q8AVK2_XENLA Q8AVK2 xenopus lae

ALIGNMENTS

RESULT 1
 Q4LE75 HUMAN
 ID Q4LE75_HUMAN PRELIMINARY; PRT; 2585 AA.
 AC Q4LE75;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE CENPE variant protein (Fragment).
 GN Name=CENPE variant protein;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Nakajima D., Saito K., Yamakawa H., Kikuno R.F., Nakayama M.,
 RA Ohara R., Okazaki N., Koga H., Nagase T., Ohara O.;
 RT "Preparation of a set of expression-ready clones of mammalian long
 RT cDNAs encoding large proteins by the ORF trap cloning method.";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB209996; BAE06078.1; -; mRNA.
 FT NON_TER 1
 SQ SEQUENCE 2585 AA; 302325 MW; 00FC4B1B2F2C7899 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 2585;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
 Db 194 RHYGETKNQRRSSRS 208
 |||||

RESULT 2
 CENPE HUMAN
 ID CENPE_HUMAN STANDARD; PRT; 2663 AA.
 AC Q02224;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Centromeric protein E (CENP-E protein).
 GN Name=CENPE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=93024922; PubMed=1406971; DOI=10.1038/359536a0;
 RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
 RT "CENP-E is a putative kinetochore motor that accumulates just before
 RT mitosis.";
 RL Nature 359:536-539 (1992).
 RN [2]
 RP CHARACTERIZATION.
 RA Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
 RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
 RT microtubule motor.";
 RL EMBO J. 14:918-926 (1995).
 RN [3]
 RP CHARACTERIZATION.
 RA Chan G.K.T., Schaar B.T., Yen T.J.;
 RT "Characterization of the kinetochore binding domain of CENP-E reveals
 RT interactions with the kinetochore proteins CENP-F and hBUBR1.";
 RL J. Cell Biol. 143:49-63 (1998).
 RN [4]
 RP FARNESYLATION
 RA Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong L.,
 RA Bishop W.R., Kirschmeier P.;
 RT "Farnesyl transferase inhibitors block the farnesylation of CENP-E and
 RT CENP-F and alter the association of CENP-E with the microtubules.";
 RL J. Biol. Chem. 275:30451-30457 (2000).
 CC -!- FUNCTION: Minus-end directed microtubule motor. Probable
 CC kinetochore motor. Accumulates just before mitosis at the G2 phase
 CC of the cell cycle. Probably important for chromosome movement
 CC and/or spindle elongation.
 CC -!- SUBUNIT: Interacts with CENP-F and BUBR1 kinase.
 CC -!- SUBCELLULAR LOCATION: Associates with kinetochores during
 CC congression, relocates to the spindle midzone at anaphase, and is
 CC quantitatively discarded at the end of the cell division.
 CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
 CC -!- SIMILARITY: Contains 1 kinesin-motor domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; Z15005; CAA78727.1; -; mRNA.
 DR FIR; S28261; S28261.
 DR PDB; 1P5C; X-ray; A/B=2-342.
 DR Ensembl; ENSG00000138778; Homo sapiens.
 DR HGNC; HGNC:1856; CENPE.
 DR MIM; 117143; -;
 DR GO; GO:0000776; C:kinetochore; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0003777; F:microtubule motor activity; TAS.
 DR GO; GO:0000067; P:DNA replication and chromosome cycle; TAS.
 DR GO; GO:0007079; P:mitotic chromosome movement towards spindle. . .; TAS.
 DR GO; GO:0000089; P:mitotic metaphase; TAS.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; TAS.
 DR InterPro; IPR001752; Kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PRO0380; KINESINHEAVY.
 DR SMART; SM00129; KISG; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
 KW 3D-structure; ATP-binding; Cell cycle; Cell division; Centromere;
 KW Coiled coil; Lipoprotein; Microtubule; Mitosis; Motor protein;
 KW Nucleotide-binding; Prenylation.
 FT DOMAIN 1 335 Kinesin-motor.
 FT NP_BIND 86 93 ATP (By similarity).
 FT REGION 2472 2663 Globular (Potential).
 FT COILED 336 2471 Potential.
 FT LIPID 2660 2660 S-farnesyl cysteine.

SQ SEQUENCE 2663 AA; 312090 MW; CEFC13880C8C8CB8 CRC64;
 Query Match 100.0%; Score 79; DB 1; Length 2663;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 189 RHYGETKNQSRSS 203
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RESULT 3
 Q4SEM9_TETNG PRELIMINARY; PRT; 1558 AA.
 AC Q4SEM9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF14615, whole genome shotgun sequence.
 GN ORFNames=GSTENG0019474001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattellio L., Poullain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype".
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAE01014615; CAG00903.1; -; Genomic DNA.
 SQ SEQUENCE 1558 AA; 179215 MW; 2B3AF13FC9DFB39D CRC64;

Query Match 94.9%; Score 75; DB 2; Length 1558;
 Best Local Similarity 93.3%; Pred. No. 0.00012;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 195 RHYGETKNQSRSS 209
 |||||:|||||

RESULT 4
 Q35059_MOUSE PRELIMINARY; PRT; 160 AA.
 AC Q35059;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Motor domain of KIF10 (Fragment).
 GN Name=Cenpe;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Murioidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ICR;
 RX MEDLINE=97420736; PubMed=9275178; DOI=10.1073/pnas.94.18.9654;
 RA Nakagawa T., Tanaka Y., Matsuoka E., Kondo S., Okada Y., Noda Y.,
 RA Kanai Y., Hirokawa N.;
 RT "Identification and classification of 16 new kinesin superfamily (KIF)
 RT proteins in mouse genome";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9654-9659(1997).
 DR EMBL; AB001426; BAA22386.1; -, mRNA.
 DR HSPF; F71119; IF9V.
 DR SMR; O35059; 1-154.
 DR Ensembl; ENSMUSG0000045328; Mus musculus.
 DR MGI; MGI:1098230; Cenpe.
 DR GO; GO:0000776; C:kinetochore; IDA.
 DR GO; GO:0008608; P:attachment of spindle microtubules to kinet. . .; TAS.
 DR InterPro; IPR001752; Kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 FT NON_TER 1
 FT NON_TER 160
 SQ SEQUENCE 160 AA; 18406 MW; 9B6E4F6E2642C241 CRC64;

Query Match 89.9%; Score 71; DB 2; Length 160;
 Best Local Similarity 93.3%; Pred. No. 4.6e-05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 108 RHYGETKNQSRSS 122
 |||||:|||||

RESULT 5
 Q7TPX4_MOUSE PRELIMINARY; PRT; 549 AA.
 AC Q7TPX4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cenpe protein (Fragment).
 GN Name=Cenpe;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Murioidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Egg;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Egg;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC052843; AAHS2843.1; -, mRNA.
DR HSSP: P17119; 1F9T.
DR SMR: Q7TPX4; 4-339.
DR Ensembl; ENSMUSG00000045328; Mus musculus.
DR MGI: MGI:1098230; Cenpe.
DR GO: GO:0000776; C:kinetochore; IDA.
DR GO: GO:0008608; P:attachment of spindle microtubules to kinet. . .; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 549 549
SQ SEQUENCE 549 AA; 62899 MW; B707C97DCFB38D3 CRC64;

Query Match 89.9%; Score 71; DB 2; Length 549;
Best Local Similarity 93.3%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
||||| ||||| |||||
DB 189 RHYGITKNQRRSSRS 203

RESULT 6
ID Q6RT24 MOUSE PRELIMINARY; PRT; 2474 AA.
AC Q6RT24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Centromere associated protein-E.
GN Name=Cenpe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22806743; PubMed=12925705; DOI=10.1083/jcb.200303167;
RA Weaver B.A., Bonday Z.Q., Putkey F.R., Kops G.J., Silk A.D.,
RA Cleveland D.W.;
RT "Centromere-associated protein-E is essential for the mammalian
RT mitotic checkpoint to prevent aneuploidy due to single chromosome
RT loss.";
RL J. Cell Biol. 162:551-563(2003).
DR EMBL: AY493378; AAR85498.1; -, mRNA.
DR SMR; Q6RT24; 4-339.
DR Ensembl; ENSMUSG00000045328; Mus musculus.
DR MGI: MGI:1098230; Cenpe.
DR GO: GO:0000776; C:kinetochore; IDA.
DR GO: GO:0008608; P:attachment of spindle microtubules to kinet. . .; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR002345; Lipocalin.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 2474 AA; 286525 MW; BAF52DD6068A2903 CRC64;

Query Match 89.9%; Score 71; DB 2; Length 2474;
Best Local Similarity 93.3%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
||||| ||||| |||||
DB 189 RHYGITKNQRRSSRS 203

RESULT 7
ID Q42263 XENLA PRELIMINARY; PRT; 2954 AA.
AC Q42263;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein.
GN Name=XENP-E;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98028574; PubMed=9363944; DOI=10.1016/S0092-8674(00)80419-5;
RA Wood K.W., Sakowicz R., Goldstein L.S., Cleveland D.W.;
RT "CENP-E is a plus end-directed kinetochore motor required for
RT metaphase chromosome alignment.";
RL Cell 91:357-366(1997).
DR EMBL: AF027728; AAC60300.1; -, mRNA.
DR PIR; T14156; T14156.
DR HSSP; P17119; 1F9T.
DR SMR; Q42263; 6-339.
DR GO: GO:0005874; C:microtubule; IEA.
DR GO: GO:0005875; C:microtubule associated complex; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003777; F:microtubule motor activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 2954 AA; 339968 MW; 439804ED0E592679 CRC64;

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
||||| ||||| |||||
DB 187 RHYGITKNQRRSSRS 201

RESULT 8
ID Q94HV9 ARATH PRELIMINARY; PRT; 807 AA.
AC Q94HV9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin motor protein (kin2), putative.
GN Name=TAM14.11;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
OX NCBI_TaxID=3702;
RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P., T.V.,
 RA Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feldblyum T.V.,
 RA White O., Fraser C.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AC027036; AAK62792.1; -, Genomic_DNA.
 DR HSP, P20480; IN6M.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 807 AA; 91261 MW; FD7CDAD68EA30C28 CRC64;
 Query Match 73.4%; Score 58; DB 2; Length 807;
 Best Local Similarity 73.3%; Pred. No. 0.095; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 184 RHFGTNNVHSSRS 198
 RESULT 9
 Q9S7P3 ARATH PRELIMINARY; PRT; 823 AA.
 AC Q9S7P3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Kinesin-like protein.
 GN Name=ZCF125;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Ooe H., Kato A., Komeda Y.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE-20018192; PubMed-10548732; DOI=10.1016/S0378-1119(99)00403-5;
 RA Kato A., Suzuki M., Kuwahara A., Ooe H., Higano-Inaba K., Komeda Y.;
 RT "Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana
 RT genomic region located around the 100 map unit of chromosome 1.";
 RL Gene 239:309-316(1999).
 DR EMBL; A5028470; BAA88114.1; -, Genomic_DNA.
 DR EMBL; A5028468; BAA88112.1; -, mRNA.
 DR FIR; T52425; T52425.
 DR HSP, P20480; IN6M.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.

DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 823 AA; 93149 MW; 6AFB1C622B4632C9 CRC64;
 Query Match 73.4%; Score 58; DB 2; Length 823;
 Best Local Similarity 73.3%; Pred. No. 0.098; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 184 RHFGTNNVHSSRS 198
 RESULT 10
 Q9LQ62 ARATH PRELIMINARY; PRT; 888 AA.
 AC Q9LQ62;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE T30516.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
 RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
 RA Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Lueros S.,
 RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
 RA Federspiel N.A., Theologis A., Ecker J.R.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC009317; AAF79747.1; -, Genomic_DNA.
 DR FIR; D96619; D96619.
 DR HSP, P20480; IN6M.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 888 AA; 100695 MW; 0D640FBACEE01B5 CRC64;
 Query Match 73.4%; Score 58; DB 2; Length 888;
 Best Local Similarity 73.3%; Pred. No. 0.11; Mismatches 1; Indels 3; Gaps 0;
 Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 215 RHFGTNNVHSSRS 229

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RESULT 11
Q7Q5F1 ANOQA
ID Q7Q5F1_ANOQA PRELIMINARY; PRT; 842 AA.
AC Q7Q5F1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000013488 (Fragment).
GN ORFNames=ENSANG0000010999;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]_TaxID=180454;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008960; BAAL1882.2; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:ATP binding; IEA.
DR GO; GO:0003777; F:ATP binding; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 842
SQ SEQUENCE 842 AA; 95303 MW; 745DB46FA1CDBCCC CRC64;

Query Match 68.4%; Score 54; DB 2; Length 842;
Best Local Similarity 73.3%; Pred. No. 0.58;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
Db 125 RKIGTNNERSRS 139

RESULT 12
Q6IWZ2 LEIDO
ID Q6IWZ2_LEIDO PRELIMINARY; PRT; 859 AA.
AC Q6IWZ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kinesin related protein (Fragment).
OS Leishmania donovani.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KE16;
RG Sivakumar R., Singh S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY615886; AAT40474.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.

QY 1 RHYGETKNQSSRS 15
Db 125 RKIGTNNERSRS 139

RESULT 13
Q6IWZ1 LEIDO
ID Q6IWZ1_LEIDO PRELIMINARY; PRT; 890 AA.
AC Q6IWZ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kinesin related protein (Fragment).
OS Leishmania donovani.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DD8;
RG Sivakumar R., Singh S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY615887; AAT40475.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:ATP binding; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR InterPro; IPR002029; Pept_S8_S53.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS00138; SUBTILASE SER; UNKNOWN 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 890
SQ SEQUENCE 890 AA; 98733 MW; 1AFF4AFD0F905407 CRC64;

Query Match 68.4%; Score 54; DB 2; Length 890;
Best Local Similarity 73.3%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
Db 240 RHTASTKNDRSSRS 254

RESULT 14
KINL_LEICH
ID KINL_LEICH STANDARD; PRT; 955 AA.
AC P46865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kinesin-like protein K39 (Fragment).
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DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 859
SQ SEQUENCE 859 AA; 95591 MW; 7F941034DA6A2155 CRC64;

Query Match 68.4%; Score 54; DB 2; Length 859;
Best Local Similarity 73.3%; Pred. No. 0.59;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
Db 241 RHTASTKNDRSSRS 255
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RESULT 13
Q6IWZ1 LEIDO
ID Q6IWZ1_LEIDO PRELIMINARY; PRT; 890 AA.
AC Q6IWZ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kinesin related protein (Fragment).
OS Leishmania donovani.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DD8;
RG Sivakumar R., Singh S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY615887; AAT40475.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:ATP binding; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR002029; Pept_S8_S53.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS00138; SUBTILASE SER; UNKNOWN 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 890
SQ SEQUENCE 890 AA; 98733 MW; 1AFF4AFD0F905407 CRC64;
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Query Match 68.4%; Score 54; DB 2; Length 890;
Best Local Similarity 73.3%; Pred. No. 0.62;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
Db 240 RHTASTKNDRSSRS 254

RESULT 14
KINL_LEICH
ID KINL_LEICH STANDARD; PRT; 955 AA.
AC P46865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kinesin-like protein K39 (Fragment).
```

GN Names=KIN;
 OS Leishmania chagasi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=44211;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=MHOM/BR/82/BA-2;
 RX MEDLINE=93133867; PubMed=8421715;
 RA Burns J.M. Jr., Shreffler W.G., Benson D.R., Ghalib H.W., Badaro R.,
 RT Reed S.G.;
 RT "Molecular characterization of a kinesin-related antigen of Leishmania
 chagasi that detects specific antibody in African and American
 visceral leishmaniasis";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
 CC -!- DEVELOPMENTAL STAGE: Predominant in anastigotes.
 CC -!- SIMILARITY: Belongs to the kinesin-like protein family.
 CC -!- SIMILARITY: Contains 1 kinesin-motor domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; L07879; AAA29254.1; -; Genomic_DNA.
 DR PIR; A47334; A47334.
 DR HSP; P17119; 3KAR.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubule; Motor protein;
 KW Nucleotide-binding; Repeat.
 FT DOMAIN 1 399 Kinesin-motor.
 FT REPEAT 704 742 1.
 FT REPEAT 743 781 2.
 FT REPEAT 782 820 3.
 FT REPEAT 821 859 4.
 FT REPEAT 860 898 5.
 FT REPEAT 899 937 6.
 FT REPEAT 938 955 7. (partial).
 FT NP_BIND 122 129 ATP (potential).
 FT REGION 704 >955 7 X 39 AA approximate tandem repeats.
 FT COILED 426 >955 Potential.
 FT NON_TER 955 955
 SQ SEQUENCE 955 AA; 106168 MW; 8CA76815BE84C6E9 CRC64;
 Query Match 68.4%; Score 54; DB 1; Length 955;
 Best Local Similarity 73.3%; Pred. No. 0.67;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 241 RHTASTKMNDRSSRS 255
 RESULT 15
 Q57UD0_9TRYP PRELIMINARY; PRT; 1803 AA.
 AC Q57UD0;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=TB927.7.3830;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=GUTat10.1;

RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostettler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC159454; AAX70789.1; -; Genomic DNA.
 SQ SEQUENCE 1803 AA; 206481 MW; 440DEAD009C0E67A CRC64;
 Query Match 68.4%; Score 54; DB 2; Length 1803;
 Best Local Similarity 73.3%; Pred. No. 1.5;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 256 RHTASTKMNDRSSRS 270
 RESULT 16
 Q57V46_9TRYP PRELIMINARY; PRT; 578 AA.
 ID Q57V46;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Kinesin, putative.
 GN ORFNames=TB927.3.3400;
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GUTat10.1;
 RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostettler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC159446; AAX70522.1; -; Genomic_DNA.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR002198; ADH short.
 DR InterPro; IPR001752; Kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
 DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
 SQ SEQUENCE 578 AA; 63787 MW; 1A0AD46C254E449D CRC64;
 Query Match 67.1%; Score 53; DB 2; Length 578;
 Best Local Similarity 73.3%; Pred. No. 0.57;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSSRS 15
 DB 201 ROKGETKNQSSRS 215
 RESULT 17
 Q57V47_9TRYP PRELIMINARY; PRT; 591 AA.
 ID Q57V47;
 AC Q57V47;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Kinesin, putative.
 GN ORFNames=TB927.3.3390;
 OS Trypanosoma brucei.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 ON NCBI_TaxID=5691;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-GUTRat10.1;
 RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
 RA Shallow J., Hou L., Djikeng A., Feldblum T., Hostetler J.,
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC159446; AAX70521.1; -; Genomic DNA.
 SQ SEQUENCE 591 AA; 65845 MW; 82B4E0AE6582B4EB CRC64;
 Query Match 67.1%; Score 53; DB 2; Length 591;
 Best Local Similarity 73.3%; Pred. No. 0.58;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQRSRS 15
 Db |||||||:
 201 RQGETKNQTSRS 215
 RESULT 18
 Q4QFW3 LEIMA
 ID Q4QFW3 LEIMA PRELIMINARY; PRT; 1229 AA.
 AC Q4QFW3
 DT 13-SEP-2005 (TreeBLrel. 31, Created)
 DT 13-SEP-2005 (TreeBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TreeBLrel. 31, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=LmjF14.1110;
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 ON NCBI_TaxID=5664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Beriman M., Blackwell J.,
 RA Smith D., Collins M., Foeker N., Harris D., Oliver K., O'Neil S.,
 RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
 RA Bianchetti G., Borzym K., Bothé G., Bruschi C., Clarioni L.,
 RA Duesterhoeft A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
 RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
 RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
 RA Tostato V., Volckaert G., Wambut R., Wedler H., Zimmermann M.,
 RA Rajandream M., and Barrall B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT005253; CAJ03171.1; -; Genomic DNA.
 SQ SEQUENCE 1229 AA; 137506 MW; 91EA1D70A2BAF92F CRC64;
 Query Match 67.1%; Score 53; DB 2; Length 1229;
 Best Local Similarity 73.3%; Pred. No. 1.4;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RHYGETKNQRSRS 15
 Db |||||||:
 211 RHTAATKNDRSSRS 225
 RESULT 19
 Q5VK10 DROME
 ID Q5VK10 DROME PRELIMINARY; PRT; 2013 AA.
 AC Q9VK10
 DT 01-MAY-2000 (TreeBLrel. 13, Created)
 DT 01-MAY-2000 (TreeBLrel. 16, Last sequence update)
 DT 01-MAY-2004 (TreeBLrel. 26, Last annotation update)
 DE CG6392-PA.
 GN Name=cnet; ORFNames=CG6392;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster."
 Science 287:2183-2195(2000).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 "Finishing a whole-genome shotgun: release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective."
 Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Scapleton M., Paclet J., Park S., Svirskas R., Smith E.,
 Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN NUCLEOTIDE SEQUENCE.
 RP FlyBase;
 RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003631; AAF53088.2; -; Genomic DNA.
 DR HSP; P17119; 1F9T.
 DR FlyBase; FBgn0040232; cmet.
 DR GO; GO:0000776; C:kinetochore; IDA.
 DR GO; GO:0000940; C:outer kinetochore of condensed chromosome; NAS.
 DR GO; GO:0007049; P:cell cycle; IMP.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; IMP.
 DR InterPro; IPR000074; ApoA1_A4_E.
 DR InterPro; IPR001752; kinesin_motor.
 DR PRINTS; PF00225; Kinesin; 1.
 DR SMART; SM00129; KISC; 1.
 DR SMART; SM00150; SPEC; 3.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 2013 AA; 231110 MW; 8A1A46581EF4F5F CRC64;

Query Match 67.1%; Score 53; DB 2; Length 2013;
 Best Local Similarity 73.3%; Pred. No. 2.6;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
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 DB 183 RTVGETNNERSRS 197

RESULT 20
 QNCGO DROME PRELIMINARY; PRT; 2244 AA.
 AC QNCGO;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Kinesin-like kinetochore motor protein CENP-meta.
 GN Name=cmet; ORFNames=CG6392;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=20351410; PubMed=10893249; DOI=10.1083/jcb.150.1.1;
 RX Yudel J.K., Marszalek J.D., McIntosh J.R., Goldstein L.S.B.,
 RA Cleveland D.W., Philip A.V.;
 RA "CENP-meta, an essential kinetochore protein required for the
 RT maintenance of metaphase chromosome alignment in Drosophila.";
 RL J. Cell Biol. 150:1-11(2000).
 DR EMBL; AF20353; AAF32355.1; -; mRNA.
 DR HSP; P17119; 1F9T.
 DR FlyBase; FBgn0040232; cmet.
 DR GO; GO:0000776; C:kinetochore; IDA.
 DR GO; GO:0000940; C:outer kinetochore of condensed chromosome; NAS.
 DR GO; GO:0007049; P:cell cycle; IMP.
 DR GO; GO:0007080; P:mitotic metaphase plate congression; IMP.
 DR InterPro; IPR000074; ApoA1_A4_E.

DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 2244 AA; 257994 MW; FA6AA3B2A541ADE0 CRC64;
 Query Match 67.1%; Score 53; DB 2; Length 2244;
 Best Local Similarity 73.3%; Pred. No. 2.9;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RHYGETKNQSRSS 15
 |||||:|||||
 DB 183 RTVGETNNERSRS 197

RESULT 21
 Q4QFM4_LEIMA
 ID Q4QFM4 LEIMA PRELIMINARY; PRT; 2765 AA.
 AC Q4QFM4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=LmjF14.1100;
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
 RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
 RA Bianchetti G., Borzym K., Bothe G., Bruschi C., Clarioni L.,
 RA Dusterhoef A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
 RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Pohl T.,
 RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
 RA Tosato V., Volckaert G., Wambutt R., Wedler H., Zimmermann M.,
 RA Rajandream M., and Barrell B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT005253; CAJ03170.1; -; Genomic DNA.
 SQ SEQUENCE 2765 AA; 301723 MW; C781913539345FA CRC64;

Query Match 67.1%; Score 53; DB 2; Length 2765;
 Best Local Similarity 73.3%; Pred. No. 3.8;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 |||||:|||||
 DB 241 RHTAATKNDSSRS 255

RESULT 22
 Q4QFM2_LEIMA
 ID Q4QFM2 LEIMA PRELIMINARY; PRT; 2976 AA.
 AC Q4QFM2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Kinesin K39, putative.
 GN ORFNames=LmjF14.1120;
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
 RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,

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RA Bianchetti G., Borzym K., Bothe G., Bruschi C., Ciarloni L.,
RA Dueterhoeft A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
RA Klages S., Kube M., Marra M., Masny D., Mueller-Auer S., Pohl T.,
RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
RA Toato V., Volckaert G., Wambutt R., Wedler H., Zimmermann M.,
RA Rajandream M., and Barrall B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CTO05253; CAJ03172.1; -; Genomic DNA.
SQ SEQUENCE 2976 AA; 341140 MW; 0283F8FB4848050D CRC64;

Query Match 67.1%; Score 53; DB 2; Length 2976;
Best Local Similarity 73.3%; Pred. No. 4.1;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
||| ||| ||| ||| |||
Db 185 RHTAATKNDRSSRS 199

RESULT 23
ID O54722_RAT PRELIMINARY; PRT; 168 AA.
AC O54722;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KRP5 (Fragment).
GN Name=Krp5; Synonyms=kRPs;
OS Rattus norvegicus (Rat)...
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Testes;
RX MEDLINE=96228687; PubMed=8688559;
RA Sperry A.O.; Zhao L.-P.;
RT "Kinesin-related proteins in the mammalian testes: candidate motors
RT for meiosis and morphogenesis";
RL Mol. Biol. Cell 7:289-305(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Testes;
RA Sperry A.O.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035954; AAB8702.1; -; mRNA.
DR HSSP; P17119; IF9V.
DR Ensembl; ENSRNOG0000019257; Rattus norvegicus.
DR RGD; 621071; Krp5.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:macrofilament motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR SMART; SM00129; KISc; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON TER 1
FT NON TER 168
SQ SEQUENCE 168 AA; 18752 MW; D961E4CDBDAAAB7 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
||| ||| ||| ||| |||
Db 114 RHTGTTQNHSSRS 128

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RESULT 24
Q9SS30_ARATH PRELIMINARY; PRT; 459 AA.
AC Q9SS30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative kinesin-like centromere protein.
GN Name=F14P13.22;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009400; AAF02823.1; -; Genomic DNA.
DR HSSP; P17119; IF9T.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISc; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 459 AA; 51872 MW; 7C8487E9B7038E6A CRC64;

Query Match 65.8%; Score 52; DB 2; Length 459;
Best Local Similarity 73.3%; Pred. No. 0.67;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
||| ||| ||| ||| |||
Db 182 RHIGETNNLYSSRS 196

RESULT 25
Q57XT2_9TRYP PRELIMINARY; PRT; 810 AA.
AC Q57XT2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Kinesin, putative.
GN ORFNames=fb927.7-7120;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallow J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wauless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC159412; AAX69587.1; -; Genomic DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.

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DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 SQ SEQUENCE 810 AA; 87881 MW; B04AF497EAD787B4 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 810;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 449 RHVGSTAVNQSRSS 463
 ||| | : ||| |

RESULT 26
 Q95LL1 MACFA
 ID Q95LL1 MACFA PRELIMINARY; PRT; 865 AA.
 AC Q95LL1;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein (Crab eating macaque)
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinæ; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Testis;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
 RA Terao K., Sugano S., Hashimoto K.;
 RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
 in the human genome sequence."
 RL BMC Genomics 3:36-36(2002).
 DR EMBL; AB072777; BAB69746.1; -; mRNA.
 DR HSP; P33173; I15S.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; UNKNOWN_1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Hypothetical protein; Microtubule; Motor protein;
 NW Nucleotide-binding.
 FT NON_TER 865
 SQ SEQUENCE 865 AA; 98464 MW; 13341B786F48324 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 865;
 Best Local Similarity 66.7%; Pred. No. 1.4;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 193 RHTGTQNEHSSRS 207
 ||| | : ||| |

RESULT 27
 Q7PCK6 MACFA
 ID Q7PCK6 MACFA PRELIMINARY; PRT; 1266 AA.
 AC Q7PCK6;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Kinesin-related protein KIF27.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinæ; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
 RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
 RA Williams S.C.;
 RT "Gene discovery in the hamster: a comparative genomics approach for
 gene annotation by sequencing of hamster testis cDNAs."
 RL BMC Genomics 4:22-22(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DDJB third party annotation (TPA) entry.
 DR EMBL; BK001055; DAA01313.1; -; mRNA.
 DR HSP; P33173; I15S.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; UNKNOWN_1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 1266 AA; 144457 MW; DES8A8EB65CC6E CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1266;
 Best Local Similarity 66.7%; Pred. No. 2.3;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
 DB 193 RHTGTQNEHSSRS 207
 ||| | : ||| |

RESULT 28
 Q86VHO HUMAN
 ID Q86VHO HUMAN PRELIMINARY; PRT; 1304 AA.
 AC Q86VHO;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE KIF27C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
 RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
 RA Williams S.C.;
 RT "Gene discovery in the hamster: a comparative genomics approach for
 gene annotation by sequencing of hamster testis cDNAs."
 RL BMC Genomics 4:22-22(2003).
 DR EMBL; AY237538; AAP04415.1; -; mRNA.
 DR HSP; P33173; I15S.
 DR EMBL; ENSG00000165115; Homo sapiens.
 DR GO; GO:0005874; C:Microtubule; IEA.
 DR GO; GO:0005875; C:Microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:Microtubule motor activity; IEA.
 DR GO; GO:0007018; P:Microtubule-based movement; IEA.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; Kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; UNKNOWN_1.
 DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.

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SQ SEQUENCE 1304 AA; 148978 MW; 7FEBD1BBC879016C CRC64;
Query Match 65.8%; Score 52; DB 2; Length 1304;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
|||:|:|:|
Db 193 RHTGTTQMHSSRS 207

RESULT 29
Q86VH1_HUMAN
ID Q86VH1 HUMAN PRELIMINARY; PRT; 1335 AA.
AC Q86VH1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIF27B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
DR EMBL; AY237537; AAP04414.1; -; mRNA.
DR HSP; P33173; I15S.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1335 AA; 152314 MW; D3D02A926D9E823F CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1335;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
|||:|:|:|
Db 193 RHTGTTQMHSSRS 207

RESULT 30
Q7M6Z5_RAT
ID Q7M6Z5 RAT PRELIMINARY; PRT; 1394 AA.
AC Q7M6Z5
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KIF27A.
GN Name=LOC306736;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
|||:|:|:|
Db 193 RHTGTTQMHSSRS 207

RESULT 31
Q7M6Z4_MOUSE
ID Q7M6Z4 MOUSE PRELIMINARY; PRT; 1394 AA.
AC Q7M6Z4
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KIF27A.
GN Name=Kif27;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
DR EMBL; BK001056; DAA01314.1; -; mRNA.
DR HSP; P33173; I15S.
DR Ensembl; ENSMUSG00000060176; Mus musculus.
DR MG; MG1:1922300; Kif27.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1394 AA; 158880 MW; 78E6AA7FF01C7987 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
|||:|:|:|
Db 193 RHTGTTQMHSSRS 207

RESULT 31
Q7M6Z4_MOUSE
ID Q7M6Z4 MOUSE PRELIMINARY; PRT; 1394 AA.
AC Q7M6Z4
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KIF27A.
GN Name=Kif27;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
DR EMBL; BK001056; DAA01314.1; -; mRNA.
DR HSP; P33173; I15S.
DR Ensembl; ENSMUSG00000060176; Mus musculus.
DR MG; MG1:1922300; Kif27.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1394 AA; 158880 MW; 78E6AA7FF01C7987 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
|||:|:|:|
Db 193 RHTGTTQMHSSRS 207

RESULT 31
Q7M6Z4_MOUSE
ID Q7M6Z4 MOUSE PRELIMINARY; PRT; 1394 AA.
AC Q7M6Z4
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein KIF27A.
GN Name=Kif27;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
DR EMBL; BK001056; DAA01314.1; -; mRNA.
DR HSP; P33173; I15S.
DR Ensembl; ENSMUSG00000060176; Mus musculus.
DR MG; MG1:1922300; Kif27.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1394 AA; 158880 MW; 78E6AA7FF01C7987 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
|||:|:~:~:~
Db 193 RHTGTTQMHSSRS 207
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SQ SEQUENCE 1394 AA; 158956 MW; AC5F7CCD2CA61D6B CRC64;
Query Match 65.8%; Score 52; DB 2; Length 1394;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
|||:|||||
Db 193 RHTGTTQNNHSSRS 207

RESULT 32
Q86VH2 HUMAN
ID Q86VH2_HUMAN PRELIMINARY; PRT; 1401 AA.
AC Q86VH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE KIF27A [OTTHUMP0000021559].
GN Name=KIF27; Synonyms=RP11-575L7.3; ORFNames=RP11-575L7.3-001;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22730772; PubMed=12783626; DOI=10.1186/1471-2164-4-22;
RA Oduru S., Campbell J.L., Karri S., Hendry W.J., Khan S.A.,
RA Williams S.C.;
RT "Gene discovery in the hamster: a comparative genomics approach for
RT gene annotation by sequencing of hamster testis cDNAs.";
RL BMC Genomics 4:22-22(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Beasley H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY237536; AAP04413.1; -; mRNA.
DR EMBL; AL354733; CA116013.1; -; Genomic_DNA.
DR HSSP; P33173; 1158.
DR Ensembl; ENSG00000165115; Homo sapiens.
DR HGNC; HGNC:18632; KIF27.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1401 AA; 160283 MW; 4563BA414C30DB21 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1401;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
|||:|||||
Db 193 RHTGTTQNNHSSRS 207

RESULT 33
Q9NCF9 DROME
ID Q9NCF9_DROME PRELIMINARY; PRT; 1931 AA.
AC Q9NCF9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitotic kinesin-like motor protein CENP-ana.

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GN Name=cana; ORFNames=CG4831;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20351410; PubMed=10893249; DOI=10.1083/jcb.150.1.1;
RA Yucel J.K., Marszalek J.D., McIntosh J.R., Goldstein L.S.B.,
RA Cleveland D.W., Philip A.V.;
RT "CENP-meta, an essential kinetochore kinesin required for the
RT maintenance of metaphase chromosome alignment in Drosophila.";
RL J. Cell Biol. 150:1-11(2000).
DR EMBL; AF220354; AAF32356.1; -; mRNA.
DR HSSP; P17119; IF9T.
DR FlyBase; FBgn0040233; cana.
DR GO; GO:0000090; P:mitotic anaphase; IMP.
DR InterPro; IPR005602; DUF334.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR ProDom; PD038149; DUF334; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1931 AA; 221863 MW; 49984D6757588D67 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1931;
Best Local Similarity 73.3%; Pred. No. 3.8;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
|||:|||||
Db 183 RVGGETNNHSSRS 197

RESULT 34
Q9VKH9 DROME
ID Q9VKH9_DROME PRELIMINARY; PRT; 1931 AA.
AC Q9VKH9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG32955-PE, isoform E.
GN Name=cana; Synonyms=CG32955; ORFNames=CG32955, CG4831;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Zhou X., Zhu S., Smith H.O.,
RA Ye J., Yeh R.-F., Zaveri J., Zhou X., Zhou X., Zhu S., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton J., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:
CC Q9VU21:CG10943; NBExp=1; IntAct=EBI-108467, EBI-108150;
DR EMBL; AE003631; AAF53089.2; -; Genomic_DNA.
DR HSSP; P17119; 1F9T.
DR IntAct; Q9VWH9; -;
DR FlyBase; FBgn0040233; cana.
DR GO; GO:0000090; P:mitotic anaphase; IMP.

DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
DR ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
KW SEQUENCE 1931 AA; 221829 MW; 5F12DD85997A71B4 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 1931;
Best Local Similarity 73.3%; Pred. No. 3.8; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 3;
QY 1 RHYGETGNQSRSS 15
DB 183 RVVGETNNERSRS 197

RESULT 35
Q9SVJ7 ARATH PRELIMINARY; PRT; 581 AA.
ID Q9SVJ7 ARATH PRELIMINARY;
AC Q9SVJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative kinesin heavy chain.
GN Name=At2g21300;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006841; AAD23678.1; -; Genomic_DNA.
DR PIR; F84599; F84599.
DR HSSP; P17119; 1F9T.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
DR SEQUENCE 581 AA; 65683 MW; 82C84CE178A311C5 CRC64;

Query Match 64.6%; Score 51; DB 2; Length 581;
Best Local Similarity 66.7%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 3;
QY 1 RHYGETGNQSRSS 15
DB 205 RKIGETSLNERSRS 219

RESULT 36
Q9SVJ8 ARATH PRELIMINARY; PRT; 834 AA.
ID Q9SVJ8 ARATH PRELIMINARY;
AC Q9SVJ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Kinesin like protein.
GN Names: F19H22.50; Synonyms: AT9g38950;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035679; CAB38815.1; -; Genomic DNA.
DR EMBL; AL161594; CAB80558.1; -; Genomic DNA.
DR PIR; T06055; T06055.
DR HSP; P31173; I158.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PSS0067; KINESIN MOTOR DOMAIN2; 1.
SQ SEQUENCE 834 AA; 94434 MW; 0A0F1835C4544C4B CRC64;
Query Match 64.6%; Score 51; DB 2; Length 834;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RHYGETQNRSSRS 15
DB 214 RKIGETSLNRSRS 228
RESULT 37
Q9VRK9 DROME
ID Q9VRK9 DROME PRELIMINARY; PRT; 677 AA.
AC Q9VRK9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE CG10642-PA.
OS Name=Klp64D; ORFNames=CG10642;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Burtis K.C., Busam D.A., Buhle H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Houten D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Hypothetical protein; Microtubule; Motor protein;
KW Nucleotide-binding.
SQ SEQUENCE 1043 AA; 112789 MW; F215D12A27628ACC CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1043;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
||| | :|||||
DB 506 RHVGATDWNERSRS 520

RESULT 40
ID Q4PG67_USTWA PRELIMINARY; PRT; 1459 AA.
AC Q4PG67;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM00896.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekova E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachihi H., Armbruster J., Bachantung P., Baldwin J., Barry A.,
RA Bayul T., Blishsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawes T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Kellis C., Kieu A., Ksner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lmbdad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalav A., Mihova T., Mikkelson T., Mienga V., Moru K.,
RA Mozes J., Multain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataravan V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zalnoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; AACP0100030; EAK82080.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1459 AA; 156992 MW; AC26C55B99645558 CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1459;
Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
||| | :|||||
DB 487 RHVGATDWNERSRS 501

RESULT 41
ID P87198_USTWA PRELIMINARY; PRT; 1459 AA.
AC P87198;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin motor protein.
GN Name=kinl;
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97361828; PubMed=9218789; DOI=10.1093/emboj/16.12.3464;
RA Lehner C., Steinberg G., Snetelaar K.M., Schliwa M., Kahmann R.,
RA Bolker M.;
RT "Identification of a motor protein required for filamentous growth in
Ustilago maydis";
RL EMBO J. 16:3464-3473(1997).
DR EMBL; U92844; AAB63336.1; -, Genomic_DNA.
DR PIR; T30196; T30196.
DR HSSP; P33173; 1I6I.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESIN_HEAVY.
DR SMART; SM00129; KISG; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1459 AA; 156933 MW; 281B74B0100F5CD0 CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1459;
Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSRSS 15
||| | :|||||
DB 487 RHVGATDWNERSRS 501

RESULT 42
ID Q9U679_STRPU PRELIMINARY; PRT; 1624 AA.
AC Q9U679;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-C.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Euechinozoa; Echinacea; Echinacea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;


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RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20027084; PubMed=10556023; DOI=10.1006/jmbi.1999.3249;
RX Rogers G.C., Hart C.L., Wedaman K.P., Scholey J.M.;
RA "Identification of kinesin-C, a calmodulin-binding carboxy-terminal
RT kinesin in animal (Strongylocentrotus purpuratus) cells.";
RL J. Mol. Biol. 294:1-8(1999).
DR EMBL; AF191095; AAF04841.1; -; mRNA.
DR HSSP; P17119; 1F9W.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; P:microtubule-based movement; IEA.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 1624 AA; 180899 MW; AAFD758487F1B7AA CRC64;

Query Match 63.3%; Score 50; DB 2; Length 1624;
Best Local Similarity 66.7%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
DB 1454 RHVASTKNSSRS 1468

RESULT 43
QI1113 MORSA
ID Q91113 MORSA PRELIMINARY; PRT; 146 AA.
AC Q91113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FKIF4 (Fragment).
GN Name=fkif4;
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bost-Uisinger L., Burnside B.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34656; AAB03190.1; -; mRNA.
DR HSSP; P20480; 1N6M.
DR GO; GO:0005874; C:microtubule associated complex; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN1; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 146
FT NON_TER 146
SQ SEQUENCE 146 AA; 16301 MW; 97D69ED068C8A8FF CRC64;

Query Match 62.0%; Score 49; DB 2; Length 146;
Best Local Similarity 60.0%; Pred. No. 0.62;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
DB 1454 RHVASTKNSSRS 1468

RESULT 44
QI1113 MORSA
ID Q91113 MORSA PRELIMINARY; PRT; 148 AA.
AC Q91113;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin motor protein KIF22 (Fragment).
GN Name=kif22;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang Z., Hanlon D.W., Marszalek J.R., Goldstein L.S.;
RL "Identification, partial characterization, and genetic mapping of
RT kinesin-like protein genes in mouse.";
RL Genomics 45:123-131(1997).
DR EMBL; AF013119; AAC39968.1; -; mRNA.
DR HSSP; P20480; 1N6M.
DR Ensembl; ENSMUSG0000030677; Mus musculus.
DR MGI; MGI:109233; Klf22.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005819; C:spindle; IEA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON_TER 148
FT NON_TER 148
SQ SEQUENCE 148 AA; 16596 MW; 0950C265C3B63EB7 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 0.63;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
DB 101 RAVGATRLNQRSSRS 115

RESULT 45
QI1113 MORSA
ID Q91113 MORSA PRELIMINARY; PRT; 156 AA.
AC Q91113;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kinesin-related protein K4 (Fragment).
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA de Hostos E.L., McCaffrey G., Vale R.D.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015713; AAB66583.1; -; Genomic_DNA.
DR HSSP; P17119; 1F9W.
DR DictyBase; DB0191404; ksnD.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
```


DR GO: GO:000524; F:ATP binding; IEA.
 DR GO: GO:0003777; F:microtubule motor activity; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR001752; Kinesin_motor.
 DR Pfam: PF00225; Kinesin; 1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE: PS00567; KINESIN MOTOR DOMAIN2; 1.
 KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 FT NON TER 1
 FT 156 156
 SQ SEQUENCE 156 AA; 17628 MW; 10A413476B343CF6 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 156;
 Best Local Similarity 66.7%; Pred. No. 0.67;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRSSRS 15
 ||| ||| ||| ||| |||
 DB 110 RHIGSTMMDSSRS 124

RESULT 46

O84JL8 ARATH
 ID O84JL8 ARATH PRELIMINARY; PRT; 193 AA.
 AC O84JL8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein Atg04985.
 GN Name:Atg04985;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BF002973; AAO22782.1; -; mRNA.
 DR EMBL; BF004413; PAA042407.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 193 AA; 21924 MW; 937EE943433684B3 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 193;
 Best Local Similarity 72.7%; Pred. No. 0.87;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RHYGETKMNQR 11
 ||| ||| ||| ||| |||
 DB 68 RHYNETRINQR 78

RESULT 47

O9MAU7 ARATH

Genoscope; Whitehead Institute Centre for Genome Research;

ID O9MAU7 ARATH PRELIMINARY; PRT; 198 AA.
 AC O9MAU7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE P13M7.2 protein.
 GN Name:P13M7.2;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu, S.,
 Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Breidel V.,
 RA Buehler E., Conway K., Feng J., Kim C., Kurtz D., Li Y.,
 RA Palm C., Shinn P., Sun H., Davis R., Ecker J., Federspiel N.,
 RA Theologis A.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Theologis;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004809; AAF40462.1; -; Genomic_DNA.
 DR PIR; E86183; E86183.
 SQ SEQUENCE 198 AA; 22437 MW; 7BBAAB2E089F9D82 CRC64;
 Query Match 62.0%; Score 49; DB 2; Length 198;
 Best Local Similarity 72.7%; Pred. No. 0.9;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RHYGETKMNQR 11
 ||| ||| ||| ||| |||
 DB 73 RHYNETRINQR 83

RESULT 48
 Q4SIJ2 TETNG
 ID Q4SIJ2 TETNG PRELIMINARY; PRT; 573 AA.
 AC Q4SIJ2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 5 SCAP14581, whole genome shotgun sequence.
 DE (Fragment).
 ORFNames=GSTENG00017667001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Bionnot C., Skallil Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RN Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RP Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; CAAG01014581; CAF99540.1; -; Genomic_DNA.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
FT NON TER 573 573
SQ SEQUENCE 573 AA; 63898 MW; 35922F1E0A592BBA CRC64;

Query Match 62.0%; Score 49; DB 2; Length 573;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
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Db 313 RHTGATQNPNSRS 327

RESULT 49

ID Q5R9A3_PONPY PRELIMINARY; PRT; 597 AA.
AC Q5R9A3.
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Hypothetical protein DKFZp45911739.
GN Name=DKFZp45911739;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Cortex.
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBSJ databases.

DR EMBL; CR859487; CAH91657.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR003583; HhH1_Bd.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00278; HhH1; 2.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Hypothetical protein; Microtubule; Motor protein;
KW Nucleotide-binding.
SQ SEQUENCE 597 AA; 66332 MW; 3F1A83D8C86F12B3 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 597;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
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Db 164 RTVGATRLNQSRSS 178

RESULT 50
Q4R838 MACFA
ID Q4R838 MACFA PRELIMINARY; PRT; 600 AA.
AC Q4R838.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Testis cDNA clone: QtsA-13558, similar to human kinesin family member
DE 22 (KIF22).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN NUCLEOTIDE SEQUENCE.
RP International consortium for macaque cDNA sequencing, analysis;
RA "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBSJ databases.
RN NUCLEOTIDE SEQUENCE.
RP Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB168622; BAE00734.1; -; mRNA.
DR InterPro; IPR003583; HhH1_Bd.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; Kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00278; HhH1; 2.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SQ SEQUENCE 600 AA; 66659 MW; 54D9132DFD291FF5 CRC64;

Query Match 62.0%; Score 49; DB 2; Length 600;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
||| |::| |
Db 164 RTVGATRLNQSRSS 178

Search completed: April 21, 2006, 13:41:59
Job time : 260 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:42:16 ; Search time 47 Seconds
(without alignments)
26.386 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGETKNQSRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	2662	2	US-09-595-684B-31
2	79	100.0	2663	2	US-09-538-092-1252
3	69	87.3	2354	2	US-09-150-867-1
4	54	68.4	955	1	US-08-006-676B-1
5	54	68.4	955	1	US-08-282-845-2
6	54	68.4	955	1	US-08-428-414A-3
7	54	68.4	955	4	PCT-US94-00324-1
8	52	65.8	341	2	US-09-724-517-4
9	52	65.8	341	2	US-09-641-807A-4
10	52	65.8	341	2	US-09-723-096-4
11	52	65.8	1279	2	US-09-724-517-2
12	52	65.8	1279	2	US-09-641-807A-2
13	52	65.8	1279	2	US-09-723-096-2
14	49	62.0	346	2	US-09-724-224-6
15	49	62.0	346	2	US-10-093-317-6
16	49	62.0	370	2	US-09-724-224-2
17	49	62.0	370	2	US-10-093-317-2
18	49	62.0	487	2	US-09-724-224-8
19	49	62.0	487	2	US-10-093-317-8
20	49	62.0	490	2	US-09-949-016-8784
21	49	62.0	512	2	US-09-724-224-4
22	49	62.0	512	2	US-10-093-317-4
23	49	62.0	665	2	US-09-595-684B-35
24	48	60.8	324	2	US-09-183-861-53
25	48	60.8	324	2	US-09-022-765-53
26	48	60.8	324	2	US-09-551-974A-53
27	48	60.8	324	2	US-09-565-501A-53

28	48	60.8	324	2	US-09-639-206A-53	Sequence 53, Appl
29	48	60.8	324	2	US-09-874-923-53	Sequence 53, Appl
30	45	57.0	411	1	US-08-713-815A-4	Sequence 4, Appl
31	45	57.0	441	1	US-08-713-815A-3	Sequence 3, Appl
32	45	57.0	915	2	US-09-949-016-7425	Sequence 7425, Ap
33	45	57.0	956	2	US-09-914-259-17	Sequence 17, Appl
34	45	57.0	957	2	US-09-914-259-16	Sequence 16, Appl
35	45	57.0	963	2	US-09-914-259-20	Sequence 20, Appl
36	45	57.0	963	2	US-09-914-259-22	Sequence 22, Appl
37	45	57.0	963	2	US-09-538-092-1060	Sequence 1060, Ap
38	45	57.0	967	2	US-09-914-259-21	Sequence 21, Appl
39	45	57.0	975	2	US-09-914-259-19	Sequence 19, Appl
40	45	57.0	978	2	US-09-949-016-10196	Sequence 10196, A
41	45	57.0	1027	2	US-09-914-259-27	Sequence 27, Appl
42	45	57.0	1031	2	US-09-914-259-24	Sequence 24, Appl
43	45	57.0	1032	2	US-09-914-259-26	Sequence 26, Appl
44	45	57.0	1032	2	US-09-538-092-1293	Sequence 1293, Ap
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46	44	55.7	706	2	US-09-914-259-29	Sequence 29, Appl
47	43	54.4	337	2	US-08-641-806-4	Sequence 4, Appl
48	43	54.4	337	2	US-09-723-129-4	Sequence 4, Appl
49	43	54.4	337	2	US-09-722-862-4	Sequence 4, Appl
50	43	54.4	342	2	US-09-641-806-2	Sequence 2, Appl
51	43	54.4	342	2	US-09-723-129-2	Sequence 2, Appl
52	43	54.4	342	2	US-09-722-862-2	Sequence 2, Appl
53	43	54.4	422	2	US-09-949-016-7927	Sequence 7927, Ap
54	43	54.4	747	2	US-09-949-016-6552	Sequence 6552, Ap
55	43	54.4	760	2	US-09-949-016-10413	Sequence 10413, A
56	42	53.2	309	2	US-09-270-767-45536	Sequence 45536, A
57	42	53.2	326	2	US-09-721-383-4	Sequence 4, Appl
58	42	53.2	326	2	US-09-721-137-4	Sequence 4, Appl
59	42	53.2	326	2	US-09-721-231-4	Sequence 4, Appl
60	42	53.2	326	2	US-10-114-764-4	Sequence 4, Appl
61	42	53.2	787	2	US-09-721-383-2	Sequence 2, Appl
62	42	53.2	787	2	US-09-721-137-2	Sequence 2, Appl
63	42	53.2	787	2	US-09-721-251-2	Sequence 2, Appl
64	42	53.2	787	2	US-10-114-764-2	Sequence 2, Appl
65	41	51.9	175	2	US-08-898-659-17	Sequence 17, Appl
66	40	50.6	205	2	US-09-637-481-2	Sequence 2, Appl
67	40	50.6	205	2	US-09-723-428-2	Sequence 2, Appl
68	40	50.6	205	2	US-09-724-520-2	Sequence 2, Appl
69	39	49.4	225	2	US-09-949-016-6768	Sequence 6768, Ap
70	39	49.4	225	2	US-08-949-016-5943	Sequence 5943, Ap
71	39	49.4	321	2	US-08-949-016-11603	Sequence 11603, A
72	39	49.4	321	2	US-09-949-016-11604	Sequence 11604, A
73	39	49.4	435	2	US-09-252-991A-24914	Sequence 24914, A
74	39	49.4	499	2	US-09-248-796A-18810	Sequence 18810, A
75	39	49.4	792	2	US-09-949-016-6199	Sequence 6199, Ap
76	39	49.4	811	2	US-08-949-016-7422	Sequence 7422, Ap
77	39	49.4	884	2	US-09-741-150-4	Sequence 4, Appl
78	39	49.4	884	2	US-10-160-187-4	Sequence 4, Appl
79	39	49.4	928	2	US-09-914-259-23	Sequence 23, Appl
80	39	49.4	1038	2	US-09-541-782-4	Sequence 4, Appl
81	39	49.4	1038	2	US-09-723-820-4	Sequence 4, Appl
82	39	49.4	1038	2	US-10-270-085-4	Sequence 4, Appl
83	38	48.1	190	2	US-09-949-016-6305	Sequence 6305, Ap
84	38	48.1	331	2	US-09-949-016-6769	Sequence 6769, Ap
85	38	48.1	375	2	US-09-572-191-4	Sequence 4, Appl
86	38	48.1	375	2	US-09-723-262-4	Sequence 4, Appl
87	38	48.1	375	2	US-09-723-219-4	Sequence 4, Appl
88	38	48.1	409	2	US-08-572-191-6	Sequence 6, Appl
89	38	48.1	409	2	US-09-723-262-6	Sequence 6, Appl
90	38	48.1	409	2	US-09-723-219-6	Sequence 6, Appl
91	38	48.1	590	2	US-09-252-991A-28989	Sequence 28989, A
92	38	48.1	880	2	US-09-949-016-7110	Sequence 7110, Ap
93	38	48.1	1388	2	US-08-572-191-2	Sequence 2, Appl
94	38	48.1	1388	2	US-09-723-262-2	Sequence 2, Appl
95	38	48.1	1388	2	US-09-723-219-2	Sequence 2, Appl
96	37	46.8	130	2	US-09-270-767-33516	Sequence 33516, A
97	37	46.8	130	2	US-09-270-767-48733	Sequence 48733, A
98	37	46.8	137	2	US-08-782-480-3	Sequence 3, Appl
99	37	46.8	137	2	US-08-954-211-3	Sequence 3, Appl
100	37	46.8	137	2	US-09-005-167A-3	Sequence 3, Appl

101	37	46.8	137	2	US-09-176-741B-3	Sequence 3, Appli	174	35	44.3	660	2	US-09-786-240-10	Sequence 10, Appli
102	37	46.8	159	1	US-08-642-406A-26	Sequence 26, Appli	175	35	44.3	660	2	US-10-012-231A-88	Sequence 88, Appli
103	37	46.8	159	2	US-09-199-534-26	Sequence 26, Appli	176	35	44.3	660	2	US-10-015-389A-88	Sequence 88, Appli
104	37	46.8	159	2	US-09-199-534-26	Sequence 26, Appli	177	35	44.3	660	2	US-10-006-768A-88	Sequence 88, Appli
105	37	46.8	159	2	US-09-491-322-26	Sequence 26, Appli	178	35	44.3	660	2	US-10-015-671A-88	Sequence 88, Appli
106	37	46.8	265	2	US-09-248-796A-16478	Sequence 16478, A	179	35	44.3	660	2	US-10-011-393A-88	Sequence 88, Appli
107	37	46.8	308	2	US-09-248-796A-20449	Sequence 20449, A	180	35	44.3	660	2	US-10-011-833A-88	Sequence 88, Appli
108	37	46.8	311	2	US-09-248-796A-16958	Sequence 16958, A	181	35	44.3	660	2	US-10-006-041A-88	Sequence 88, Appli
109	37	46.8	457	2	US-09-902-540-11961	Sequence 11961, A	182	35	44.3	660	2	US-10-012-064A-88	Sequence 88, Appli
110	37	46.8	563	2	US-09-248-796A-18632	Sequence 18632, A	183	35	44.3	677	2	US-10-101-464A-891	Sequence 891, App
111	37	46.8	578	2	US-09-489-039A-10599	Sequence 10599, A	184	35	44.3	678	2	US-09-595-684B-25	Sequence 25, Appl
112	37	46.8	627	2	US-09-360-545-32	Sequence 32, Appli	185	35	44.3	706	2	US-09-949-016-11444	Sequence 11444, A
113	37	46.8	694	2	US-09-270-767-36948	Sequence 36948, A	186	35	44.3	784	2	US-09-724-586A-1	Sequence 1, Appli
114	37	46.8	694	2	US-09-270-767-52165	Sequence 52165, A	187	35	44.3	784	2	US-09-600-823-1	Sequence 1, Appli
115	37	46.8	705	2	US-09-270-767-44461	Sequence 44461, A	188	35	44.3	784	2	US-09-724-666-1	Sequence 1, Appli
116	37	46.8	810	2	US-09-538-092-1275	Sequence 1275, Ap	189	35	44.3	815	2	US-09-914-259-18	Sequence 18, Appl
117	37	46.8	1474	2	US-09-677-046A-4	Sequence 4, Appli	190	35	44.3	922	2	US-09-252-991A-32759	Sequence 32759, A
118	37	46.8	1503	2	US-09-677-046A-6	Sequence 6, Appli	191	35	44.3	959	2	US-09-991A-21747	Sequence 21747, A
119	37	46.8	1509	2	US-09-677-046A-2	Sequence 2, Appli	192	35	44.3	1103	2	US-09-162-373-1	Sequence 1, Appli
120	36	45.6	61	2	US-09-513-999C-4208	Sequence 4208, Ap	193	35	44.3	1103	2	US-09-467-946-1	Sequence 9935, Ap
121	36	45.6	79	2	US-09-134-001C-3147	Sequence 3147, Ap	194	35	44.3	1123	2	US-09-949-016-9935	Sequence 46552, A
122	36	45.6	116	2	US-09-270-767-32936	Sequence 32936, A	195	35	44.3	1124	2	US-09-270-767-46552	Sequence 23, Appl
123	36	45.6	116	2	US-09-270-767-32936	Sequence 32936, A	196	35	44.3	1231	2	US-09-595-684B-23	Sequence 2, Appli
124	36	45.6	168	2	US-08-990-791-10	Sequence 10, Appl	197	35	44.3	1231	2	US-09-592-054-2	Sequence 8, Appli
125	36	45.6	168	2	US-09-372-591-10	Sequence 10, Appl	198	35	44.3	1232	2	US-09-592-054-8	Sequence 3, Appli
126	36	45.6	248	2	US-09-489-039A-14007	Sequence 60, Appl	199	35	44.3	1234	2	US-09-792-616-3	Sequence 8, Appli
127	36	45.6	248	2	US-09-050-739-60	Sequence 60, Appl	200	35	44.3	1503	2	US-09-647-140B-8	Sequence 39, Appl
128	36	45.6	361	2	US-09-596-541-2	Sequence 2, Appli	201	35	44.3	1690	2	US-09-595-684B-39	Sequence 6474, Ap
129	36	45.6	361	2	US-10-126-205-2	Sequence 2, Appli	202	35	44.3	1690	2	US-09-949-016-6474	Sequence 9887, Ap
130	36	45.6	369	2	US-09-596-541-6	Sequence 6, Appli	203	35	44.3	1695	2	US-09-949-016-9887	Sequence 5, Appli
131	36	45.6	369	2	US-09-723-595-6	Sequence 6, Appli	204	34	43.0	38	1	US-08-513-278-5	Patent No. 5514582
132	36	45.6	369	2	US-09-723-595-6	Sequence 6, Appli	205	34	43.0	38	6	5514582-5	Sequence 55128, A
133	36	45.6	369	2	US-10-126-205-6	Sequence 6, Appli	206	34	43.0	89	2	US-09-252-991A-25128	Sequence 5514582
134	36	45.6	370	2	US-09-596-541-4	Sequence 4, Appli	207	34	43.0	117	6	5514582-7	Patent No. 5514582
135	36	45.6	370	2	US-09-723-595-4	Sequence 4, Appli	208	34	43.0	119	1	US-08-340-539A-12	Sequence 12, Appl
136	36	45.6	370	2	US-10-126-205-4	Sequence 4, Appli	209	34	43.0	140	2	US-09-645-415A-60	Sequence 60, Appl
137	36	45.6	384	1	US-07-783-706-2	Sequence 2, Appli	210	34	43.0	156	2	US-09-543-681A-6616	Sequence 6616, Ap
138	36	45.6	384	1	US-08-445-342A-2	Sequence 2, Appli	211	34	43.0	164	2	US-09-270-767-40899	Sequence 40899, A
139	36	45.6	384	2	US-09-066-481-2	Sequence 2, Appli	212	34	43.0	164	2	US-09-270-767-40899	Sequence 56115, A
140	36	45.6	384	2	US-09-802-285-2	Sequence 2, Appli	213	34	43.0	233	2	US-09-543-681A-5936	Sequence 5336, Ap
141	36	45.6	384	4	PCT-US92-09124-2	Sequence 37, Appl	214	34	43.0	244	2	US-09-248-796A-16447	Sequence 16447, A
142	36	45.6	519	2	US-09-595-684B-37	Sequence 10535, Ap	215	34	43.0	254	2	US-09-489-039A-10109	Sequence 10109, A
143	36	45.6	1437	2	US-09-949-016-10535	Sequence 6899, Ap	216	34	43.0	342	2	US-09-252-991A-24027	Sequence 24027, A
144	36	45.6	1780	2	US-09-949-016-6899	Sequence 6899, Ap	217	34	43.0	366	2	US-09-718-692-4	Sequence 4, Appli
145	36	45.6	1786	2	US-09-949-016-7880	Sequence 7880, Ap	218	34	43.0	366	2	US-09-718-852-4	Sequence 4, Appli
146	35	44.3	11	1	US-08-245-853-22	Sequence 22, Appl	219	34	43.0	366	2	US-09-718-815-4	Sequence 4, Appli
147	35	44.3	11	1	US-08-573-675-22	Sequence 22, Appl	220	34	43.0	372	1	US-08-513-278-4	Sequence 4, Appli
148	35	44.3	101	2	US-09-248-796A-27613	Sequence 27613, A	221	34	43.0	372	6	5514582-4	Patent No. 5514582
149	35	44.3	119	1	US-08-340-539A-13	Sequence 13, Appl	222	34	43.0	406	2	US-09-248-796A-16921	Sequence 16921, A
150	35	44.3	137	2	US-10-101-464A-669	Sequence 669, App	223	34	43.0	421	2	US-09-107-532A-4030	Sequence 4030, Ap
151	35	44.3	143	2	US-09-270-767-32145	Sequence 32145, A	224	34	43.0	433	2	US-09-595-424-2	Sequence 2, Appli
152	35	44.3	143	2	US-09-270-767-47362	Sequence 47362, A	225	34	43.0	494	2	US-09-595-424-4	Sequence 4, Appli
153	35	44.3	167	2	US-09-270-767-46036	Sequence 46036, A	226	34	43.0	510	2	US-09-993-777-3	Sequence 3, Appli
154	35	44.3	194	2	US-09-774-639-242	Sequence 242, App	227	34	43.0	510	4	PCT-US96-03916-3	Sequence 3, Appli
155	35	44.3	260	2	US-09-270-767-41775	Sequence 41775, A	228	34	43.0	530	2	US-09-543-681A-4646	Sequence 4646, Ap
156	35	44.3	275	2	US-09-328-352-7814	Sequence 7814, Ap	229	34	43.0	560	2	US-09-270-767-44751	Sequence 44751, A
157	35	44.3	278	2	US-09-270-767-45313	Sequence 45313, A	230	34	43.0	560	2	US-09-107-532A-7053	Sequence 7053, Ap
158	35	44.3	299	2	US-09-248-796A-17636	Sequence 17636, A	231	34	43.0	611	2	US-09-902-540-14644	Sequence 14644, A
159	35	44.3	325	2	US-08-311-731A-249	Sequence 249, App	232	34	43.0	623	4	US-09-993-777-64	Sequence 64, Appl
160	35	44.3	340	2	US-09-142-593-1	Sequence 1, Appli	233	34	43.0	623	4	PCT-US96-03916-64	Sequence 64, Appl
161	35	44.3	340	2	US-09-927-886-1	Sequence 1, Appli	234	34	43.0	627	2	US-10-222-100-3	Sequence 3, Appli
162	35	44.3	404	2	US-09-328-352-6480	Sequence 6480, Ap	235	34	43.0	658	2	US-09-595-424-6	Sequence 6, Appli
163	35	44.3	412	2	US-09-347-801-21	Sequence 21, Appl	236	34	43.0	670	1	US-08-366-547-2	Sequence 2, Appli
164	35	44.3	412	2	US-09-854-731-21	Sequence 21, Appl	237	34	43.0	670	2	US-09-292-858B-2	Sequence 2, Appli
165	35	44.3	435	2	US-09-489-039A-9982	Sequence 9982, Ap	238	34	43.0	680	2	US-09-949-016-10119	Sequence 10119, A
166	35	44.3	473	2	US-09-592-054-6	Sequence 6, Appli	239	34	43.0	768	2	US-09-134-000C-6467	Sequence 6467, Ap
167	35	44.3	502	2	US-09-248-796A-16824	Sequence 16824, A	240	34	43.0	798	2	US-10-104-047-3335	Sequence 3335, Ap
168	35	44.3	522	2	US-09-592-054-4	Sequence 4, Appli	241	34	43.0	856	2	US-09-949-016-6558	Sequence 6558, Ap
169	35	44.3	632	2	US-09-976-594-41	Sequence 41, Appl	242	34	43.0	874	2	US-09-369-364A-15	Sequence 15, Appl
170	35	44.3	632	2	US-09-991-181-219	Sequence 219, App	243	34	43.0	884	2	US-09-948-016-10588	Sequence 10588, A
171	35	44.3	632	2	US-09-980-444-219	Sequence 219, App	244	34	43.0	895	2	US-09-489-039A-12499	Sequence 12499, A
172	35	44.3	632	2	US-09-987-333-219	Sequence 219, App	245	34	43.0	952	2	US-09-328-352-4551	Sequence 4551, Ap
173	35	44.3	632	2	US-09-992-598-219	Sequence 219, App	246	34	43.0	957	2	US-09-595-684B-27	Sequence 27, Appl

247	34	43.0	960	2	US-09-595-424-8	Sequence 8, Appli	Sequence 2, Appli	320	33	41.8	604	2	US-08-487-744-4	Sequence 4, Appli
248	34	43.0	1564	2	US-10-144-198-2	Sequence 2, Appli	Sequence 4, Appli	321	33	41.8	604	2	US-08-487-744-5	Sequence 5, Appli
249	34	43.0	1564	2	US-10-144-198-4	Sequence 4, Appli	Sequence 2, Appli	322	33	41.8	604	2	US-08-930-589A-18	Sequence 18, Appl
250	34	43.0	1637	2	US-09-718-852-2	Sequence 2, Appli	Sequence 2, Appli	323	33	41.8	604	2	US-09-599-781-18	Sequence 18, Appl
251	34	43.0	1637	2	US-09-718-852-2	Sequence 2, Appli	Sequence 2, Appli	324	33	41.8	604	2	US-10-027-961A-18	Sequence 18, Appl
252	34	43.0	1637	2	US-09-718-815-2	Sequence 2, Appli	Sequence 2, Appli	325	33	41.8	604	4	PCT-US93-09167-4	Sequence 4, Appli
253	34	43.0	2318	2	US-09-091-219-24	Sequence 24, Appl	Sequence 24, Appl	326	33	41.8	604	4	PCT-US93-09167-5	Sequence 5, Appli
254	34	43.0	2318	2	US-09-660-541-24	Sequence 24, Appl	Sequence 24, Appl	327	33	41.8	610	2	US-09-902-540-13312	Sequence 5, Appli
255	34	43.0	2465	1	US-08-596-291-3	Sequence 3, Appli	Sequence 3, Appli	328	33	41.8	632	2	US-09-205-658-159	Sequence 1312, A
256	34	43.0	2465	2	US-09-100-804-3	Sequence 3, Appli	Sequence 3, Appli	329	33	41.8	632	2	US-09-205-658-160	Sequence 159, App
257	34	43.0	2466	2	US-09-080-855-12	Sequence 12, Appl	Sequence 12, Appl	330	33	41.8	632	2	US-09-248-796A-19238	Sequence 160, App
258	34	43.0	2466	2	US-09-566-076-12	Sequence 12, Appl	Sequence 12, Appl	331	33	41.8	652	2	US-09-594-669-14	Sequence 19238, A
259	34	43.0	2466	4	PCT-US94-09943-2	Sequence 2, Appli	Sequence 2, Appli	332	33	41.8	723	2	US-10-112-432-14	Sequence 14, Appl
260	34	43.0	2485	2	US-09-290-640-46	Sequence 46, Appl	Sequence 46, Appl	333	33	41.8	723	2	US-09-594-669-16	Sequence 14, Appl
261	34	43.0	2485	2	US-09-665-615B-46	Sequence 46, Appl	Sequence 46, Appl	334	33	41.8	725	2	US-09-595-684B-33	Sequence 33, Appl
262	33.5	42.4	117	1	US-08-274-661B-38	Sequence 38, Appl	Sequence 38, Appl	335	33	41.8	725	2	US-10-112-432-16	Sequence 16, Appl
263	33.5	42.4	367	2	US-09-248-796A-20601	Sequence 20601, A	Sequence 20601, A	336	33	41.8	725	2	US-09-849-602-20	Sequence 20, Appl
264	33.5	42.4	372	1	US-08-513-278-2	Sequence 2, Appli	Sequence 2, Appli	337	33	41.8	867	2	US-10-197-220-109	Sequence 109, App
265	33.5	42.4	372	6	5514582-2	Patent No. 5514582	Patent No. 5514582	338	33	41.8	922	2	US-10-104-047-2694	Sequence 2694, Ap
266	33.5	42.4	385	1	US-08-340-539A-2	Sequence 2, Appli	Sequence 2, Appli	339	33	41.8	1073	2	US-09-541-782-6	Sequence 6, Appli
267	33.5	42.4	385	1	US-08-461-592B-2	Sequence 2, Appli	Sequence 2, Appli	340	33	41.8	1073	2	US-09-723-820-6	Sequence 6, Appli
268	33.5	42.4	715	2	US-09-248-796A-20602	Sequence 20602, A	Sequence 20602, A	341	33	41.8	1073	2	US-10-270-085-6	Sequence 6, Appli
269	33.5	42.4	848	2	US-09-538-092-33	Sequence 33, Appl	Sequence 33, Appl	342	33	41.8	1184	2	US-09-541-782-2	Sequence 2, Appli
270	33	41.8	23	2	US-09-537-226-13	Sequence 13, Appl	Sequence 13, Appl	343	33	41.8	1184	2	US-09-723-820-2	Sequence 2, Appli
271	33	41.8	26	1	US-08-482-142-22	Sequence 22, Appl	Sequence 22, Appl	344	33	41.8	1184	2	US-10-270-085-2	Sequence 2, Appli
272	33	41.8	26	1	US-08-478-572-22	Sequence 22, Appl	Sequence 22, Appl	345	33	41.8	1255	2	US-09-248-796A-14158	Sequence 14158, A
273	33	41.8	26	2	US-08-484-296-22	Sequence 22, Appl	Sequence 22, Appl	346	33	41.8	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
274	33	41.8	81	2	US-09-537-226-16	Sequence 16, Appl	Sequence 16, Appl	347	32.5	41.1	111	2	US-09-252-991A-26279	Sequence 26279, A
275	33	41.8	90	2	US-09-809-665A-147	Sequence 147, App	Sequence 147, App	348	32.5	41.1	122	2	US-09-248-796A-22797	Sequence 22797, A
276	33	41.8	120	2	US-09-489-039A-12045	Sequence 12045, A	Sequence 12045, A	349	32.5	41.1	122	2	US-09-248-796A-23030	Sequence 23030, A
277	33	41.8	187	2	US-09-270-767-33863	Sequence 33863, A	Sequence 33863, A	350	32.5	41.1	338	2	US-09-902-540-16254	Sequence 16254, A
278	33	41.8	188	2	US-09-270-767-34999	Sequence 34999, A	Sequence 34999, A	351	32.5	41.1	463	2	US-09-543-681A-6745	Sequence 6745, Ap
279	33	41.8	188	2	US-09-270-767-50216	Sequence 50216, A	Sequence 50216, A	352	32.5	41.1	5588	2	US-09-036-987A-6	Sequence 6, Appli
280	33	41.8	245	2	US-09-252-991A-26889	Sequence 26889, A	Sequence 26889, A	353	32.5	41.1	5588	2	US-09-370-700-6	Sequence 6, Appli
281	33	41.8	254	2	US-09-128-352-5775	Sequence 30977, A	Sequence 30977, A	354	32.5	41.1	5588	2	US-09-603-207-6	Sequence 6, Appli
282	33	41.8	259	2	US-08-663-831-2	Sequence 2, Appli	Sequence 2, Appli	355	32	40.5	16	1	US-08-476-062A-31	Sequence 31, Appl
283	33	41.8	260	2	US-09-248-796A-20535	Sequence 20535, A	Sequence 20535, A	356	32	40.5	16	4	PCT-US96-01314-31	Sequence 31, Appl
284	33	41.8	270	2	US-09-489-039A-10186	Sequence 10186, A	Sequence 10186, A	357	32	40.5	56	2	US-09-556-605-32	Sequence 32, Appl
285	33	41.8	284	2	US-09-252-991A-22267	Sequence 22267, A	Sequence 22267, A	358	32	40.5	56	2	US-08-676-124-51	Sequence 51, Appl
286	33	41.8	325	2	US-09-949-016-7282	Sequence 7282, Ap	Sequence 7282, Ap	359	32	40.5	58	2	US-09-414-878-51	Sequence 51, Appl
287	33	41.8	325	2	US-09-949-016-7282	Sequence 7282, Ap	Sequence 7282, Ap	360	32	40.5	58	2	US-09-240-136-51	Sequence 51, Appl
288	33	41.8	333	2	US-09-248-796A-19280	Sequence 19280, A	Sequence 19280, A	361	32	40.5	58	2	US-09-638-770A-51	Sequence 51, Appl
289	33	41.8	339	2	US-09-489-039A-12070	Sequence 12070, A	Sequence 12070, A	362	32	40.5	58	2	US-09-270-767-58671	Sequence 58671, A
290	33	41.8	341	2	US-09-270-767-36808	Sequence 36808, A	Sequence 36808, A	363	32	40.5	64	2	US-09-270-767-58671	Sequence 58671, A
291	33	41.8	341	2	US-09-270-767-52025	Sequence 52025, A	Sequence 52025, A	364	32	40.5	66	2	US-09-248-796A-22637	Sequence 22637, A
292	33	41.8	362	2	US-09-594-669-6	Sequence 6, Appli	Sequence 6, Appli	365	32	40.5	66	2	US-09-513-999C-7449	Sequence 7449, Ap
293	33	41.8	362	2	US-10-112-432-6	Sequence 6, Appli	Sequence 6, Appli	366	32	40.5	66	2	US-09-248-796A-26998	Sequence 26998, A
294	33	41.8	391	2	US-09-594-669-4	Sequence 4, Appli	Sequence 4, Appli	367	32	40.5	82	2	US-09-936-697-10	Sequence 10, Appl
295	33	41.8	391	2	US-10-112-432-4	Sequence 4, Appli	Sequence 4, Appli	368	32	40.5	82	2	US-09-134-001C-4887	Sequence 4887, Ap
296	33	41.8	405	2	US-09-594-669-12	Sequence 12, Appl	Sequence 12, Appl	369	32	40.5	90	2	US-09-543-681A-4385	Sequence 4385, Ap
297	33	41.8	405	2	US-10-112-432-12	Sequence 12, Appl	Sequence 12, Appl	370	32	40.5	93	2	US-09-328-352-8122	Sequence 8122, Ap
298	33	41.8	430	2	US-09-594-669-2	Sequence 2, Appli	Sequence 2, Appli	371	32	40.5	100	2	US-08-881-037-20	Sequence 20, Appl
299	33	41.8	430	2	US-10-112-432-2	Sequence 2, Appli	Sequence 2, Appli	372	32	40.5	111	2	PCT-US92-02044-4	Sequence 4, Appli
300	33	41.8	434	2	US-09-594-669-10	Sequence 10, Appl	Sequence 10, Appl	373	32	40.5	119	4	US-09-252-991A-26884	Sequence 26884, A
301	33	41.8	434	2	US-10-112-432-10	Sequence 10, Appl	Sequence 10, Appl	374	32	40.5	125	2	US-09-270-767-57534	Sequence 57534, A
302	33	41.8	437	2	US-09-538-092-109	Sequence 109, App	Sequence 109, App	375	32	40.5	127	2	US-09-556-605-3	Sequence 3, Appli
303	33	41.8	470	2	US-08-396-988-2	Sequence 2, Appli	Sequence 2, Appli	376	32	40.5	130	2	US-09-252-991A-28600	Sequence 28600, A
304	33	41.8	470	2	US-09-391-104-26	Sequence 26, Appl	Sequence 26, Appl	377	32	40.5	142	2	US-09-732-210-161	Sequence 161, App
305	33	41.8	470	2	US-09-594-669-8	Sequence 8, Appli	Sequence 8, Appli	378	32	40.5	149	2	US-09-270-767-43328	Sequence 43328, A
306	33	41.8	473	2	US-09-252-991A-25026	Sequence 25026, A	Sequence 25026, A	379	32	40.5	154	2	US-09-936-697-11	Sequence 11, Appl
307	33	41.8	473	2	US-10-112-432-8	Sequence 8, Appli	Sequence 8, Appli	380	32	40.5	173	2	US-09-270-767-41114	Sequence 41114, A
308	33	41.8	473	2	US-09-949-016-10876	Sequence 10876, A	Sequence 10876, A	381	32	40.5	173	2	US-09-270-767-56330	Sequence 56330, A
309	33	41.8	473	2	US-09-252-991A-19298	Sequence 19298, A	Sequence 19298, A	382	32	40.5	173	2	US-09-902-540-12036	Sequence 12036, A
310	33	41.8	478	2	US-09-457-040B-13	Sequence 13, Appl	Sequence 13, Appl	383	32	40.5	180	2	US-09-252-991A-24674	Sequence 24674, A
311	33	41.8	499	2	US-09-905-999-21	Sequence 21, Appl	Sequence 21, Appl	384	32	40.5	180	2	US-09-936-697-12	Sequence 12, Appl
312	33	41.8	499	2	US-09-252-991A-27436	Sequence 27436, A	Sequence 27436, A	385	32	40.5	182	2	US-09-252-991A-18626	Sequence 18626, A
313	33	41.8	506	2	US-09-489-039A-8499	Sequence 8499, Ap	Sequence 8499, Ap	386	32	40.5	191	2	US-09-270-767-38008	Sequence 38008, A
314	33	41.8	601	2	US-08-064-271-10	Sequence 10, Appl	Sequence 10, Appl	387	32	40.5	191	2	US-09-270-767-53225	Sequence 53225, A
315	33	41.8	604	1	US-08-487-753-4	Sequence 4, Appli	Sequence 4, Appli	388	32	40.5	196	2	US-09-252-991A-32026	Sequence 32026, A
316	33	41.8	604	1	US-08-487-753-4	Sequence 4, Appli	Sequence 4, Appli	389	32	40.5	215	2	US-09-270-767-37890	Sequence 37890, A
317	33	41.8	604	1	US-08-487-753-5	Sequence 5, Appli	Sequence 5, Appli	390	32	40.5	215	2	US-09-270-767-53107	Sequence 53107, A
318	33	41.8	604	1	US-08-480-065-4	Sequence 4, Appli	Sequence 4, Appli	391	32	40.5	215	2		
319	33	41.8	604	1	US-08-480-065-5	Sequence 5, Appli	Sequence 5, Appli	392	32	40.5	215	2		

393	32	40.5	217	2	US-09-107-532A-7168	Sequence 7168, Ap	466	32	40.5	688	2	US-09-949-016-11400	Sequence 11400, A
394	32	40.5	222	2	US-09-710-279-376	Sequence 376, App	467	32	40.5	715	2	US-09-543-681A-7603	Sequence 7603, Ap
395	32	40.5	223	2	US-09-134-001C-4829	Sequence 4829, Ap	468	32	40.5	720	2	US-09-583-110-2940	Sequence 2940, Ap
396	32	40.5	227	2	US-08-911-853-23	Sequence 23, Appl	469	32	40.5	720	2	US-09-107-433-4193	Sequence 4193, Ap
397	32	40.5	227	2	US-09-479-409-23	Sequence 23, Appl	470	32	40.5	746	2	US-09-949-016-10964	Sequence 10964, A
398	32	40.5	227	2	US-09-479-453-23	Sequence 23, Appl	471	32	40.5	819	2	US-09-489-039A-12105	Sequence 12105, A
399	32	40.5	243	2	US-09-640-211A-761	Sequence 761, App	472	32	40.5	830	2	US-09-064-199-19	Sequence 19, Appl
400	32	40.5	248	2	US-09-248-796A-19090	Sequence 19090, A	473	32	40.5	934	2	US-08-840-466A-19	Sequence 19, Appl
401	32	40.5	266	2	US-09-248-796A-19613	Sequence 19613, A	474	32	40.5	934	2	US-09-696-188B-19	Sequence 19, Appl
402	32	40.5	267	2	US-09-419-788-30	Sequence 30, Appl	475	32	40.5	934	2	US-10-150-058-19	Sequence 19, Appl
403	32	40.5	276	2	US-09-270-767-44401	Sequence 44401, A	476	32	40.5	934	2	US-08-837-459-19	Sequence 19, Appl
404	32	40.5	286	1	US-08-358-117-2	Sequence 2, Appl	477	32	40.5	935	2	US-09-914-259-25	Sequence 25, Appl
405	32	40.5	287	2	US-09-252-991A-30447	Sequence 30447, A	478	32	40.5	943	2	US-09-540-236-3458	Sequence 3458, Ap
406	32	40.5	309	2	US-09-107-532A-6518	Sequence 6518, Ap	479	32	40.5	950	2	US-10-009-332-1	Sequence 1, Appl
407	32	40.5	318	2	US-09-270-767-42255	Sequence 42255, A	480	32	40.5	1014	2	US-09-134-000C-6265	Sequence 6265, Ap
408	32	40.5	326	2	US-08-866-381A-2	Sequence 2, Appl	481	32	40.5	1039	2	US-09-949-016-7859	Sequence 7859, Ap
409	32	40.5	326	2	US-09-280-598-52	Sequence 52, Appl	482	32	40.5	1066	2	US-09-248-796A-15476	Sequence 15476, A
410	32	40.5	326	2	US-09-489-039A-12537	Sequence 12537, A	483	32	40.5	1066	2	US-09-541-782-8	Sequence 8, Appl
411	32	40.5	344	2	US-09-147-236-11	Sequence 11, Appl	484	32	40.5	1066	2	US-09-723-820-8	Sequence 8, Appl
412	32	40.5	344	2	US-09-522-474-11	Sequence 11, Appl	485	32	40.5	1066	2	US-10-270-085-8	Sequence 8, Appl
413	32	40.5	348	2	US-09-252-991A-23520	Sequence 23520, A	486	32	40.5	1094	1	US-08-680-326-40	Sequence 40, Appl
414	32	40.5	349	2	US-09-540-236-3199	Sequence 3199, Ap	487	32	40.5	1106	2	US-09-054-199-17	Sequence 17, Appl
415	32	40.5	362	2	US-09-252-991A-16985	Sequence 16985, A	488	32	40.5	1114	2	US-09-914-259-28	Sequence 28, Appl
416	32	40.5	362	2	US-10-104-047-2732	Sequence 2732, Ap	489	32	40.5	1114	2	US-09-949-002-550	Sequence 550, App
417	32	40.5	376	2	US-09-270-767-32753	Sequence 32753, A	490	32	40.5	1130	1	US-08-519-547A-6	Sequence 6, Appl
418	32	40.5	376	2	US-10-104-047-47970	Sequence 47970, A	491	32	40.5	1130	2	US-09-064-199-18	Sequence 18, Appl
419	32	40.5	376	2	US-10-104-047-2623	Sequence 2623, Ap	492	32	40.5	1130	2	US-09-949-002-295	Sequence 295, App
420	32	40.5	387	2	US-10-000-489-112	Sequence 112, App	493	32	40.5	1137	2	US-09-902-481B-3	Sequence 3, Appl
421	32	40.5	410	2	US-09-347-801-10	Sequence 10, Appl	494	32	40.5	1137	2	US-09-902-481B-4	Sequence 4, Appl
422	32	40.5	410	2	US-09-854-731-10	Sequence 10, Appl	495	32	40.5	1137	2	US-09-902-481B-5	Sequence 5, Appl
423	32	40.5	412	2	US-09-252-991A-17935	Sequence 17935, A	496	32	40.5	1137	2	US-09-902-481B-6	Sequence 6, Appl
424	32	40.5	412	2	US-09-270-767-42908	Sequence 42908, A	497	32	40.5	1152	1	US-08-476-062A-43	Sequence 43, Appl
425	32	40.5	437	2	US-09-248-796A-16332	Sequence 16332, A	498	32	40.5	1152	4	PCT-US96-01314-43	Patent No. 5424399
426	32	40.5	494	2	US-09-489-039A-8154	Sequence 8154, Ap	499	32	40.5	1152	6	5424399-2	Patent No. 5424399
427	32	40.5	513	1	US-08-406-855A-21	Sequence 21, Appl	500	32	40.5	1153	1	US-08-173-497-3	Sequence 3, Appl
428	32	40.5	513	2	US-09-206-899-21	Sequence 21, Appl	501	32	40.5	1153	1	US-08-286-889-3	Sequence 3, Appl
429	32	40.5	513	2	US-09-724-519-6	Sequence 6, Appl	502	32	40.5	1153	1	US-08-485-618-3	Sequence 3, Appl
430	32	40.5	513	2	US-09-592-037-6	Sequence 6, Appl	503	32	40.5	1153	1	US-08-362-652-3	Sequence 3, Appl
431	32	40.5	513	2	US-09-428-156B-6	Sequence 6, Appl	504	32	40.5	1153	1	US-08-605-672-3	Sequence 3, Appl
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434	32	40.5	515	1	US-08-722-001-25	Sequence 25, Appl	507	32	40.5	1153	2	US-09-193-043-3	Sequence 3, Appl
435	32	40.5	515	2	US-09-032-742-5	Sequence 5, Appl	508	32	40.5	1153	2	US-09-688-307A-3	Sequence 3, Appl
436	32	40.5	515	2	US-09-688-415-9	Sequence 9, Appl	510	32	40.5	1207	2	US-09-902-481B-1	Sequence 1, Appl
437	32	40.5	517	1	US-08-467-568-10	Sequence 10, Appl	511	32	40.5	1207	2	US-09-064-199-16	Sequence 16, Appl
438	32	40.5	517	1	US-09-030-582-10	Sequence 10, Appl	512	32	40.5	1886	2	US-09-538-092-915	Sequence 917, App
439	32	40.5	520	1	US-08-334-698-4	Sequence 4, Appl	513	32	40.5	1886	2	US-09-369-364A-13	Sequence 13, Appl
440	32	40.5	520	1	US-08-228-932-4	Sequence 4, Appl	514	32	40.5	1937	2	US-08-938-105-3	Sequence 3, Appl
441	32	40.5	520	1	US-08-468-939-4	Sequence 4, Appl	515	32	40.5	1937	2	US-09-538-092-918	Sequence 918, App
442	32	40.5	520	1	US-08-406-855A-4	Sequence 4, Appl	516	32	40.5	1938	2	US-09-949-016-6417	Sequence 6417, Ap
443	32	40.5	520	1	US-08-722-190-4	Sequence 4, Appl	517	32	40.5	1939	2	US-09-310-187A-1	Sequence 1, Appl
444	32	40.5	520	2	US-08-244-354-4	Sequence 4, Appl	518	32	40.5	1939	2	US-09-538-092-915	Sequence 915, App
445	32	40.5	520	2	US-09-206-899-4	Sequence 4, Appl	519	32	40.5	1939	2	US-09-538-092-917	Sequence 917, App
446	32	40.5	520	2	US-09-444-783-4	Sequence 4, Appl	520	32	40.5	1939	2	US-09-949-016-6925	Sequence 6925, Ap
447	32	40.5	520	2	US-09-688-415-4	Sequence 4, Appl	521	32	40.5	1940	2	US-09-949-016-11104	Sequence 11104, A
448	32	40.5	520	4	PCT-US95-04203-4	Sequence 4, Appl	522	32	40.5	1942	2	US-09-538-092-901	Sequence 901, App
449	32	40.5	532	2	US-09-487-558B-360	Sequence 360, App	523	32	40.5	1959	2	US-09-949-016-8134	Sequence 8134, Ap
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451	32	40.5	534	2	US-09-663-326-1	Sequence 1, Appl	525	32	40.5	2556	1	US-09-051-019-2	Sequence 2, Appl
452	32	40.5	536	2	US-09-107-532A-5507	Sequence 5507, Ap	526	32	40.5	2556	1	US-08-185-432-17	Sequence 17, Appl
453	32	40.5	575	2	US-09-724-519-8	Sequence 8, Appl	527	32	40.5	2556	1	US-08-083-590A-20	Sequence 20, Appl
454	32	40.5	575	2	US-09-592-037-8	Sequence 8, Appl	528	32	40.5	2556	2	US-08-532-384-20	Sequence 2, Appl
455	32	40.5	575	2	US-09-428-156B-8	Sequence 8, Appl	529	32	40.5	2556	2	US-08-899-232-2	Sequence 2, Appl
456	32	40.5	610	2	US-09-252-991A-24942	Sequence 24942, A	530	32	40.5	2556	2	US-09-121-457-2	Sequence 2, Appl
457	32	40.5	618	2	US-08-866-381A-6	Sequence 6, Appl	531	32	40.5	2930	2	US-09-417-822-2	Sequence 2, Appl
458	32	40.5	621	1	US-08-208-887A-49	Sequence 49, Appl	532	32	40.5	2930	2	US-09-957-837A-2	Sequence 2, Appl
459	32	40.5	621	1	US-09-280-598-18	Sequence 18, Appl	533	31.5	39.9	52	2	US-09-959-897-50	Sequence 50, Appl
460	32	40.5	621	2	US-08-945-771-4	Sequence 4, Appl	534	31.5	39.9	338	2	US-09-634-957-4	Sequence 4, Appl
461	32	40.5	626	2	US-09-252-991A-20268	Sequence 20268, A	535	31.5	39.9	338	2	US-09-723-153-4	Sequence 4, Appl
462	32	40.5	637	1	US-10-100-252-4	Sequence 4, Appl	536	31.5	39.9	338	2	US-09-723-429-4	Sequence 4, Appl
463	32	40.5	673	1	US-08-455-073A-6	Sequence 6, Appl	537	31.5	39.9	392	2	US-09-796-487-6	Sequence 6, Appl
464	32	40.5	677	2	US-09-252-991A-32924	Sequence 32924, A	538	31.5	39.9	415	2	US-09-784-810C-15	Sequence 15, Appl

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543	31.5	39.9	790	2	US-09-723-429-2	Sequence 2, Appl1	616	31	39.2	316	2	US-09-252-991A-21428	Sequence 21428, A
544	31.5	39.9	938	2	US-10-104-047-3855	Sequence 3855, Ap	617	31	39.2	317	2	US-09-540-236-3830	Sequence 3830, Ap
545	31	39.2	54	2	US-09-270-767-56761	Sequence 56761, A	618	31	39.2	319	2	US-09-724-510-2	Sequence 2, Appl1
546	31	39.2	60	2	US-09-248-796A-24618	Sequence 24618, A	619	31	39.2	319	2	US-09-723-216-2	Sequence 2, Appl1
547	31	39.2	71	2	US-09-143-470-20	Sequence 20, Appl1	620	31	39.2	319	2	US-09-675-227-2	Sequence 2, Appl1
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549	31	39.2	75	2	US-09-328-352-8019	Sequence 8019, Ap	622	31	39.2	340	2	US-09-949-016-7280	Sequence 7280, Ap
550	31	39.2	73	2	US-09-621-976-6909	Sequence 6909, Ap	623	31	39.2	343	2	US-09-967-908A-8	Sequence 8, Appl1
551	31	39.2	89	2	US-09-248-796A-20387	Sequence 20387, A	624	31	39.2	343	2	US-10-159-151-8	Sequence 8, Appl1
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554	31	39.2	101	2	US-09-021-976-4910	Sequence 4910, Ap	627	31	39.2	362	2	US-09-252-991A-31349	Sequence 31349, A
555	31	39.2	101	2	US-10-004-860-1124	Sequence 1124, Ap	628	31	39.2	363	2	US-09-967-908A-10	Sequence 10, Appl1
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562	31	39.2	111	2	US-08-649-006A-2	Sequence 2, Appl1	635	31	39.2	380	2	US-09-638-937-11	Sequence 11, Appl1
563	31	39.2	111	2	US-09-771-023-2	Sequence 2, Appl1	636	31	39.2	380	2	US-09-248-796A-16419	Sequence 16419, A
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565	31	39.2	119	2	US-09-513-999C-6717	Sequence 6717, Ap	638	31	39.2	381	2	US-10-159-151-6	Sequence 6, Appl1
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568	31	39.2	130	2	US-09-248-796A-14186	Sequence 14186, A	641	31	39.2	388	2	US-09-270-767-61007	Sequence 61007, A
569	31	39.2	131	1	US-08-466-583-6	Sequence 6, Appl1	642	31	39.2	389	2	US-09-725-945-2	Sequence 2, Appl1
570	31	39.2	131	2	US-08-265-427-6	Sequence 6, Appl1	643	31	39.2	394	2	US-08-791-115B-27	Sequence 27, Appl1
571	31	39.2	131	4	PCT-US95-07820-6	Sequence 6, Appl1	644	31	39.2	394	2	US-09-140-749-17	Sequence 17, Appl1
572	31	39.2	140	2	US-09-902-540-10461	Sequence 10461, A	645	31	39.2	397	2	US-08-991-426-4	Sequence 4, Appl1
573	31	39.2	145	1	US-08-470-179-32	Sequence 32, Appl1	646	31	39.2	397	2	US-09-143-470-4	Sequence 4, Appl1
574	31	39.2	159	2	US-09-640-211A-818	Sequence 818, Ap	647	31	39.2	397	2	US-08-649-006A-4	Sequence 4, Appl1
575	31	39.2	162	2	US-09-199-637A-431	Sequence 431, Ap	648	31	39.2	397	2	US-09-252-991A-26558	Sequence 26558, A
576	31	39.2	162	2	US-09-270-767-33851	Sequence 33851, A	649	31	39.2	397	2	US-09-771-023-4	Sequence 4, Appl1
577	31	39.2	162	2	US-09-270-767-42123	Sequence 42123, A	650	31	39.2	403	2	US-08-791-115B-1	Sequence 1, Appl1
578	31	39.2	162	2	US-09-270-767-48068	Sequence 48068, A	651	31	39.2	403	2	US-08-791-115B-23	Sequence 23, Appl1
579	31	39.2	171	2	US-09-605-703B-1696	Sequence 1696, Ap	652	31	39.2	403	2	US-08-791-115B-25	Sequence 25, Appl1
580	31	39.2	173	2	US-09-328-352-8078	Sequence 8078, Ap	653	31	39.2	403	2	US-09-140-749-2	Sequence 2, Appl1
581	31	39.2	189	2	US-09-216-393B-130	Sequence 130, Ap	654	31	39.2	403	2	US-09-140-749-10	Sequence 10, Appl1
582	31	39.2	189	2	US-09-538-092-553	Sequence 533, Ap	655	31	39.2	403	2	US-09-140-749-49	Sequence 49, Appl1
583	31	39.2	193	1	US-08-438-439C-21	Sequence 21, Appl1	656	31	39.2	403	2	US-09-140-749-55	Sequence 55, Appl1
584	31	39.2	193	2	US-09-270-767-57892	Sequence 57892, A	657	31	39.2	403	2	US-09-140-749-57	Sequence 57, Appl1
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594	31	39.2	243	2	US-09-270-767-62302	Sequence 62302, A	667	31	39.2	430	2	US-08-791-115B-7	Sequence 7, Appl1
595	31	39.2	248	2	US-09-248-796A-27704	Sequence 27704, A	668	31	39.2	430	2	US-09-140-749-18	Sequence 18, Appl1
596	31	39.2	249	2	US-09-205-658-309	Sequence 309, Ap	669	31	39.2	439	2	US-09-248-796A-15968	Sequence 15968, A
597	31	39.2	250	2	US-09-248-796A-23347	Sequence 23347, A	670	31	39.2	445	2	US-10-104-047-2209	Sequence 2209, Ap
598	31	39.2	251	2	US-09-270-767-41536	Sequence 41536, A	671	31	39.2	455	2	US-09-252-991A-18265	Sequence 18265, A
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602	31	39.2	266	2	US-09-252-991A-20635	Sequence 20635, A	675	31	39.2	462	2	US-08-468-161-1	Sequence 1, Appl1
603	31	39.2	268	2	US-09-248-796A-14566	Sequence 14566, A	676	31	39.2	462	2	US-09-051-759-1	Sequence 1, Appl1
604	31	39.2	270	2	US-09-809-920-12	Sequence 12, Appl1	677	31	39.2	462	4	PCT-US95-08156-1	Sequence 1, Appl1
605	31	39.2	271	2	US-09-318-794A-2	Sequence 2, Appl1	678	31	39.2	464	2	US-08-970-134-3	Sequence 3, Appl1
606	31	39.2	271	2	US-09-318-793A-4	Sequence 4, Appl1	679	31	39.2	466	2	US-08-970-134-1	Sequence 1, Appl1
607	31	39.2	272	2	US-09-069-023-24	Sequence 24, Appl1	680	31	39.2	466	2	US-09-605-703B-2816	Sequence 2816, Ap
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686	31	39.2	518	2	US-09-206-551-45	Sequence 45, Appl	759	1180	2	US-09-153-757-8	Sequence 8, Appli
687	31	39.2	523	2	US-09-949-016-11263	Sequence 11263, A	760	1180	2	US-09-459-715-8	Sequence 8, Appli
688	31	39.2	526	2	US-09-910-174B-9	Sequence 9, Appli	761	1212	1	US-08-072-574-10	Sequence 10, Appl
689	31	39.2	526	2	US-09-620-461-9	Sequence 9, Appli	762	1212	1	US-08-486-270-10	Sequence 10, Appl
690	31	39.2	526	2	US-09-949-016-6122	Sequence 6122, Ap	763	1212	2	US-08-367-264-10	Sequence 10, Appl
691	31	39.2	533	2	US-09-360-197-10	Sequence 10, Appl	764	1212	2	US-08-660-148-5	Sequence 5, Appli
692	31	39.2	534	2	US-09-949-016-8945	Sequence 8945, Ap	765	1212	2	US-09-153-757-10	Sequence 10, Appl
693	31	39.2	534	2	US-09-613-486-44	Sequence 44, Appl	766	1212	2	US-09-459-715-10	Sequence 10, Appl
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695	31	39.2	540	2	US-09-949-016-11644	Sequence 11644, A	768	1212	2	US-09-949-016-9879	Sequence 9879, Ap
696	31	39.2	553	2	US-09-949-016-10648	Sequence 10648, A	769	1368	2	US-09-967-908A-2	Sequence 2, Appli
697	31	39.2	559	2	US-09-140-749-15	Sequence 15, Appl	770	1368	2	US-10-159-151-2	Sequence 2, Appli
698	31	39.2	564	2	US-09-949-016-11234	Sequence 11234, A	771	1839	1	US-09-172-977-4	Sequence 4, Appli
699	31	39.2	565	2	US-08-908-156A-12	Sequence 12, Appl	772	1839	2	US-09-404-108-4	Sequence 4, Appli
700	31	39.2	571	1	US-07-958-905A-25	Sequence 25, Appl	773	2753	2	US-09-949-016-7659	Sequence 7659, Ap
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705	31	39.2	597	2	US-09-140-749-8	Sequence 8, Appli	778	2753	2	US-09-538-092-1246	Sequence 1246, Ap
706	31	39.2	598	2	US-09-270-767-46086	Sequence 46086, A	779	2753	2	US-09-538-092-1246	Sequence 1246, Ap
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708	31	39.2	607	2	US-09-949-016-6293	Sequence 6293, Ap	781	2753	2	US-09-538-092-1246	Sequence 1246, Ap
709	31	39.2	616	2	US-09-248-796A-14992	Sequence 14992, A	782	2753	2	US-09-538-092-1246	Sequence 1246, Ap
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711	31	39.2	645	2	US-09-328-501-1	Sequence 1, Appli	784	2753	2	US-09-538-092-1246	Sequence 1246, Ap
712	31	39.2	645	2	US-08-791-115B-6	Sequence 6, Appli	785	2753	2	US-09-538-092-1246	Sequence 1246, Ap
713	31	39.2	646	2	US-09-777-710A-1	Sequence 1, Appli	786	2753	2	US-09-538-092-1246	Sequence 1246, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 31, Application US/09595684B
; Patent No. 654766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Ohashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaiebzig, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
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; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-31

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Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 1252, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542

US-09-538-092-1252
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
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; PRIOR FILING DATE: 1999-04-01
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; NUMBER OF SEQ ID NOS: 1387
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US-09-538-092-1252

Query Match 100.0%; Score 79; DB 2; Length 2663;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 1, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150,867
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: PRT
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
; OTHER INFORMATION: member of the kinesin superfamily of microtubule
; OTHER INFORMATION: motor proteins
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(472)
; OTHER INFORMATION: kinesin like motor domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (473)..(2752)
; OTHER INFORMATION: rod domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2753)..(2954)
; OTHER INFORMATION: tail domain
US-09-150-867-1

Query Match 87.3%; Score 69; DB 2; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRSSRS 15
```

```
Db      187 RHYGETKMDHSSRS 201
|||||
RESULT 4
US-08-006-676B-1
; Sequence 1, Application US/08006676B
; Patent No. 5411865
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; TITLE OF INVENTION: Diagnosis of Leishmaniasis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jeffrey B. Oster
; STREET: 8339 SE 57th Street
; CITY: Mercer Island
; STATE: Washington
; COUNTRY: USA
; ZIP: 98040-4906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/006,676B
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oster, Jeffrey B.
; REGISTRATION NUMBER: 32,585
; REFERENCE/DOCKET NUMBER: REED-4
; TELEPHONE: (206) 232 7845
; TELEFAX: (206) 236 0205
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-006-676B-1

Query Match      68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMDHSSRS 15
|||
Db      241 RHTASTKMDHSSRS 255
|||||

RESULT 5
US-08-282-845-2
; Sequence 2, Application US/08282845
; Patent No. 5719263
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: A 230kd Antigen Present in Leishmania
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Macintosh Operating System 7.1
; SOFTWARE: Microsoft Word for Macintosh 5.1a

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,845
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Kadlecak, Ann T.
; REGISTRATION NUMBER: 39,244
; REFERENCE/DOCKET NUMBER: 210121.407
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-428-414A-3

Query Match      68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMDHSSRS 15
|||
Db      241 RHTASTKMDHSSRS 255
|||||

RESULT 6
US-08-428-414A-3
; Sequence 3, Application US/08428414A
; Patent No. 5912166
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: LEISHMANIASIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,414A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Kadlecak, Ann T.
; REGISTRATION NUMBER: 39,244
; REFERENCE/DOCKET NUMBER: 210121.407
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-428-414A-3
```

Query Match 68.4%; Score 54; DB 1; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 241 RHTASTKMDRRSSRS 255

RESULT 7
PCT-US94-00324-1
; Sequence 1, Application PC/TUS9400324
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; TITLE OF INVENTION: Diagnosis of Leishmaniasis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/006,676
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 5004-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 955 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-00324-1
Query Match 68.4%; Score 54; DB 4; Length 955;
Best Local Similarity 73.3%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 241 RHTASTKMDRRSSRS 255

RESULT 8
US-09-724-517-4
; Sequence 4, Application US/09724517
; Patent No. 6379941
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/724,517
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-724-517-4

Query Match 65.8%; Score 52; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 192 RHTGTQWNEHSSRS 206

RESULT 9
US-09-641-807A-4
; Sequence 4, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6440731el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641,807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-641-807A-4

Query Match 65.8%; Score 52; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15
DB 192 RHTGTQWNEHSSRS 206

RESULT 10
US-09-723-096-4
; Sequence 4, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6448026el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723,096
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-723-096-4

Query Match 65.8%; Score 52; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSSRS 15


```
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-6

Query Match          62.0%; Score 49; DB 2; Length 346;
Best Local Similarity 66.7%; Pred. No. 0.66;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 208 RTVGATRLNQSRSS 222

RESULT 16
US-09-724-224-2
; Sequence 2, Application US/09724224
; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-09-724-224-2

Query Match          62.0%; Score 49; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 0.71;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 232 RTVGATRLNQSRSS 246

RESULT 17
US-10-093-317-2
; Sequence 2, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-2

Query Match          62.0%; Score 49; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 0.71;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 232 RTVGATRLNQSRSS 246

RESULT 18
US-09-724-224-8
; Sequence 8, Application US/09724224
; Patent No. 6387644
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6387644el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/09/724,224
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-09-724-224-8

Query Match          62.0%; Score 49; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 0.96;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 208 RTVGATRLNQSRSS 222

RESULT 19
US-10-093-317-8
; Sequence 8, Application US/10093317
; Patent No. 6762043
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: No. 6762043el motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/093,317
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/724,224
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-10-093-317-8

Query Match          62.0%; Score 49; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 0.96;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 208 RTVGATRLNQSRSS 222

RESULT 20
US-09-949-016-8784
; Sequence 8784, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C0001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8784
/ LENGTH: 490
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-8784

Query Match          62.0%; Score 49; DB 2; Length 490;
Best Local Similarity 66.7%; Pred. No. 0.96;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRSSRS 15
DB      240 RTVGATRLNQRRSSRS 254

RESULT 21
US-09-724-224-4
/ Sequence 4, Application US/09724224
/ Patent No. 6387644
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ TITLE OF INVENTION: No. 6387644el motor proteins and methods for
/ TITLE OF INVENTION: their use
/ FILE REFERENCE: 1044
/ CURRENT APPLICATION NUMBER: US/09/724,224
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/597,292
/ PRIOR FILING DATE: 2000-06-20
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Human
US-09-724-224-4

Query Match          62.0%; Score 49; DB 2; Length 512;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRSSRS 15
DB      233 RTVGATRLNQRRSSRS 247

RESULT 22
US-10-093-317-4
/ Sequence 4, Application US/10093317
/ Patent No. 6762043
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ TITLE OF INVENTION: No. 6762043el motor proteins and methods for
/ TITLE OF INVENTION: their use
/ FILE REFERENCE: 1044
/ CURRENT APPLICATION NUMBER: US/10/093,317
/ PRIOR FILING DATE: 2002-03-06
/ PRIOR APPLICATION NUMBER: 09/724,224
/ PRIOR FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 8
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Human
US-10-093-317-4

Query Match          62.0%; Score 49; DB 2; Length 512;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRSSRS 15
DB      233 RTVGATRLNQRRSSRS 247

RESULT 23
US-09-595-684B-35
/ Sequence 35, Application US/09595684B
/ Patent No. 6544766
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Ohashi, Cara
/ APPLICANT: Sakowicz, Roman
/ APPLICANT: Vaisberg, Eugeni
/ APPLICANT: Wood, Kenneth
/ APPLICANT: Yu, Ming
/ TITLE OF INVENTION: Human kinesins and methods of producing
/ TITLE OF INVENTION: and purifying human kinesins
/ FILE REFERENCE: CYTOP036
/ CURRENT APPLICATION NUMBER: US/09/595,684B
/ CURRENT FILING DATE: 2002-06-24
/ PRIOR APPLICATION NUMBER: 09/295,612
/ PRIOR FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 105
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 665
/ TYPE: PRT
/ ORGANISM: Human
US-09-595-684B-35

Query Match          62.0%; Score 49; DB 2; Length 665;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRRSSRS 15
DB      232 RTVGATRLNQRRSSRS 246

RESULT 24
US-09-183-861-53
/ Sequence 53, Application US/09183861
/ Patent No. 6365165
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skelky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
```



```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-565-501A-53

```

```

Query Match 60.8%; Score 48; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 RHYGETKMQRSRS 15
   || || || || ||
Db 234 RHTAATKFNDRSRS 248

```

```

RESULT 28
US-09-639-206A-53
; Sequence 53, Application US/09639206A
; Patent No. 661337
; GENERAL INFORMATION:

```

```

; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-639-206A-53

```

```

Query Match 60.8%; Score 48; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 RHYGETKMQRSRS 15
   || || || || ||
Db 234 RHTAATKFNDRSRS 248

```

```

RESULT 29
US-09-874-923-53
; Sequence 53, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:

```

```

; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark

```

```

; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Leishmania chagasi
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(324)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-874-923-53

```

```

Query Match 60.8%; Score 48; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 RHYGETKMQRSRS 15
   || || || || ||
Db 234 RHTAATKFNDRSRS 248

```

```

RESULT 30
US-08-713-815A-4
; Sequence 4, Application US/08713815A
; Patent No. 5830659
; GENERAL INFORMATION:
; APPLICANT: Russell J. Stewart
; TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: AST Ascentia 900N
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,815A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T3214/U-2202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-713-815A-4

```

```

Query Match 57.0%; Score 45; DB 1; Length 411;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 RHYGETKMQRSRS 15
   || || || || ||
Db 197 RHIAVTNNHRSRS 211

```

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RESULT 31
US-08-713-815A-3
; Sequence 3, Application US/08713815A
; Patent No. 5830659
; GENERAL INFORMATION:
; APPLICANT: Russell J. Stewart
; TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
; TITLE OF INVENTION: SEPARATIONS BY KINESINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: AST Ascentia 900N
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,815A
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T3214/U-2202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-713-815A-3

Query Match 57.0%; Score 45; DB 1; Length 441;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 197 RHIAVTNNNEHSRS 211

RESULT 32
US-09-949-016-7425
; Sequence 7425, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7425
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7425

Query Match 57.0%; Score 45; DB 1; Length 441;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 197 RHIAVTNNNEHSRS 211

RESULT 33
US-09-914-259-17
; Sequence 17, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-17

Query Match 57.0%; Score 45; DB 2; Length 956;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 191 RHVAVTNNNEHSRS 205

RESULT 34
US-09-914-259-16
; Sequence 16, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-16

Query Match 57.0%; Score 45; DB 2; Length 957;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMNQSRSS 15
Db 191 RHVAVTNNNEHSRS 205

RESULT 35
US-09-914-259-20
; Sequence 20, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
```

```
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-20

Query Match      57.0%; Score 45; DB 2; Length 963;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 36
US-09-914-259-22
; Sequence 22, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Loligo pealeii
US-09-914-259-21

Query Match      57.0%; Score 45; DB 2; Length 967;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 39
US-09-914-259-19
; Sequence 19, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 975
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-914-259-19

Query Match      57.0%; Score 45; DB 2; Length 975;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 197 RHVAVTNMNEHSRS 211
```

```
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-20

Query Match      57.0%; Score 45; DB 2; Length 963;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 36
US-09-914-259-22
; Sequence 22, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-22

Query Match      57.0%; Score 45; DB 2; Length 963;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 190 RHVAVTNMNEHSRS 204

RESULT 37
US-09-538-092-1060
; Sequence 1060, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurPatSeqFormatter Version 0.9
; SEQ ID NO 1060
; LENGTH: 963
; TYPE: PRT
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RESULT 40
US-09-949-016-10196
; Sequence 10196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10196
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10196

Query Match          57.0%; Score 45; DB 2; Length 978;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 205 RHVAVTNMNEHSRS 219

RESULT 41
US-09-914-259-27
; Sequence 27, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-27

Query Match          57.0%; Score 45; DB 2; Length 1027;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 191 RHVAVTNMNEHSRS 205

RESULT 42
US-09-914-259-24
; Sequence 24, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
```

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; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1031
; TYPE: PRT
; ORGANISM: Strongylocentrotus purpuratus
US-09-914-259-24

Query Match          57.0%; Score 45; DB 2; Length 1031;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 189 RHVAVTNMNEHSRS 203

RESULT 43
US-09-914-259-26
; Sequence 26, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-26

Query Match          57.0%; Score 45; DB 2; Length 1032;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 5; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
|||:||||
Db 191 RHVAVTNMNEHSRS 205

RESULT 44
US-09-538-092-1293
; Sequence 1293, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqformatter Version 0.9
; SEQ ID NO 1293
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Homo sapiens
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
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; OTHER INFORMATION: Polypeptide Accession Number Q12840
US-09-538-092-1293

Query Match          57.0%; Score 45; DB 2; Length 1032;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRRSSRS 15
   ||| ||| ||| |||
Db 191 RHVAVTNMEHSRS 205

RESULT 45
US-09-252-991A-26189
; Sequence 26189, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26189
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26189

Query Match          55.7%; Score 44; DB 2; Length 683;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRRSSRS 15
   ||| ||| ||| |||
Db 176 RHRGTGROGRRS 190

RESULT 46
US-09-914-259-29
; Sequence 29, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-914-259-29

Query Match          55.7%; Score 44; DB 2; Length 706;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRRSSRS 15
   ||| ||| ||| |||
Db 330 RKIGETDYNARRSSRS 344

RESULT 47
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US-09-641-806-4
; Sequence 4, Application US/09641806
; Patent No. 6395527
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6395527el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/641,806
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-641-806-4

Query Match          54.4%; Score 43; DB 2; Length 337;
Best Local Similarity 60.0%; Pred. No. 7.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRRSSRS 15
   ||| ||| ||| |||
Db 190 RHTGATHLNHLSSRS 204

RESULT 48
US-09-723-129-4
; Sequence 4, Application US/09723129
; Patent No. 6551787
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6551787el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/723,129
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/641,806
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-723-129-4

Query Match          54.4%; Score 43; DB 2; Length 337;
Best Local Similarity 60.0%; Pred. No. 7.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQRRSSRS 15
   ||| ||| ||| |||
Db 190 RHTGATHLNHLSSRS 204

RESULT 49
US-09-722-862-4
; Sequence 4, Application US/09722862
; Patent No. 6562610
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6562610el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/722,862
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/641,806
; PRIOR FILING DATE: 2000-08-17
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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-09-722-862-4

Query Match 54.4%; Score 43; DB 2; Length 337;
Best Local Similarity 60.0%; Pred. No. 7.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMQRSRS 15
|||:||||
Db 190 RHTGATHLNLSSRS 204

RESULT 50
US-09-641-806-2
; Sequence 2, Application US/09641806
; Patent No. 6395527
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6395527el motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1034
; CURRENT APPLICATION NUMBER: US/09/641,806
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Human
US-09-641-806-2

Query Match 54.4%; Score 43; DB 2; Length 342;
Best Local Similarity 60.0%; Pred. No. 8;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKMQRSRS 15
|||:||||
Db 191 RHTGATHLNLSSRS 205

Search completed: April 21, 2006, 13:43:19
Job time : 56 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:53:21 ; Search time 164 Seconds
(without alignments)
38.216 Million cell updates/sec

Title: US-09-993-399-1

Perfect score: 79

Sequence: 1 RHYGTQNRSSRS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata1/pubpaa/us07_PUBCOMB.pep:*

2: /cgn2_6/ptodata1/pubpaa/us08_PUBCOMB.pep:*

3: /cgn2_6/ptodata1/pubpaa/us09_PUBCOMB.pep:*

4: /cgn2_6/ptodata1/pubpaa/us10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata1/pubpaa/us10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata1/pubpaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	355	US-10-517-510-4	Sequence 4, Appl1
2	79	100.0	496	US-10-517-510-2	Sequence 2, Appl1
3	79	100.0	2503	US-10-828-985A-11	Sequence 11, Appl1
4	79	100.0	2543	US-10-828-985A-9	Sequence 9, Appl1
5	79	100.0	2568	US-10-828-985A-7	Sequence 7, Appl1
6	79	100.0	2633	US-10-450-763-36864	Sequence 36864, A
7	79	100.0	2663	US-10-723-860-749	Sequence 749, App
8	69	87.3	2954	US-10-650-280-1	Sequence 1, Appl1
9	65	82.3	668	US-10-425-115-263022	Sequence 263022, A
10	65	82.3	694	US-10-425-114-59725	Sequence 59725, A
11	63	79.7	201	US-10-437-963-116808	Sequence 116808, A
12	53	67.1	2013	US-10-097-143-13758	Sequence 13758, A
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14	52	65.8	182	US-10-437-963-176714	Sequence 176714, App
15	52	65.8	1401	US-10-287-226-142	Sequence 142, App
16	52	65.8	1931	US-10-097-143-9828	Sequence 9828, Ap
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21	49	62.0	370	US-10-797-893-2	Sequence 2, Appl1
22	49	62.0	460	US-09-925-300-1228	Sequence 1228, Ap
23	49	62.0	487	US-10-797-893-8	Sequence 8, Appl1
24	49	62.0	490	US-10-334-143-80	Sequence 80, Appl
25	49	62.0	512	US-10-797-893-4	Sequence 4, Appl1
26	49	62.0	665	US-10-733-878-425	Sequence 425, App
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34	47	59.5	78	4	US-10-425-115-201216	Sequence 201216, A
35	47	59.5	247	4	US-10-424-599-156142	Sequence 156142, A
36	47	59.5	272	4	US-10-424-599-274019	Sequence 274019, A
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41	46	58.2	788	4	US-10-437-963-173884	Sequence 173884, A
42	46	58.2	932	4	US-10-473-276-1	Sequence 1, Appl1
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52	45	57.0	957	4	US-10-080-608A-16	Sequence 16, Appl
53	45	57.0	957	4	US-10-370-685-105	Sequence 105, App
54	45	57.0	963	4	US-10-080-608A-20	Sequence 20, Appl
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58	45	57.0	965	4	US-10-437-963-169150	Sequence 169150, A
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62	45	57.0	975	4	US-10-370-685-108	Sequence 108, App
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68	45	57.0	1031	4	US-10-080-608A-24	Sequence 24, Appl
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71	45	57.0	1032	4	US-10-370-685-115	Sequence 115, App
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78	44	55.7	303	4	US-10-425-115-361734	Sequence 361734, A
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83	44	55.7	706	4	US-10-370-685-118	Sequence 118, App
84	44	55.7	706	4	US-10-369-493-22469	Sequence 22469, A
85	44	55.7	709	4	US-10-425-115-351144	Sequence 351144, A
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87	44	55.7	800	4	US-10-424-599-187507	Sequence 187507, A
88	44	55.7	804	4	US-10-437-963-183489	Sequence 183489, A
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91	44	55.7	967	4	US-10-425-114-62697	Sequence 62697, A
92	44	55.7	1147	4	US-10-437-963-104637	Sequence 104637, A
93	44	55.7	1462	4	US-10-437-963-158098	Sequence 158098, A
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95	43	54.4	672	4	US-10-408-765A-1664	Sequence 1664, Ap
96	43	54.4	915	4	US-10-437-963-112350	Sequence 112350, A
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98	43	54.4	954	4	US-10-473-276-2	Sequence 2, Appl1
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103	43	54.4	1062	4	US-10-345-072-37	Sequence 37, Appl	176	38	48.1	215	4	US-10-221-625-88	Sequence 88, Appl
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114	42	53.2	1006	4	US-10-437-963-147933	Sequence 147933, A	187	38	48.1	409	4	US-10-332-089-6	Sequence 6, Appli
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117	42	53.2	1218	6	US-11-097-143-30399	Sequence 30399, A	190	38	48.1	484	4	US-10-425-115-347146	Sequence 347146, A
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124	41	51.9	542	4	US-10-424-599-242324	Sequence 242324, A	197	38	48.1	663	5	US-10-811-080-14	Sequence 14, Appl
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126	41	51.9	605	4	US-10-425-115-242819	Sequence 242819, A	199	38	48.1	718	4	US-10-282-122A-76979	Sequence 76979, A
127	41	51.9	658	4	US-10-425-114-54318	Sequence 54318, A	200	38	48.1	992	5	US-10-739-930-7903	Sequence 7903, Ap
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129	41	51.9	703	4	US-10-425-115-253968	Sequence 253968, A	202	38	48.1	1030	4	US-10-425-114-62748	Sequence 62748, A
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133	41	51.9	1014	4	US-10-437-963-156793	Sequence 156793, A	206	38	48.1	1388	4	US-10-173-999-32	Sequence 32, Appl
134	41	51.9	1045	4	US-10-437-963-150217	Sequence 150217, A	207	38	48.1	1388	4	US-10-332-089-2	Sequence 2, Appli
135	41	51.9	1080	4	US-10-437-963-142399	Sequence 142399, A	208	38	48.1	1388	4	US-10-188-832-164	Sequence 164, App
136	41	51.9	252	4	US-10-437-963-179734	Sequence 129734, A	209	38	48.1	1388	5	US-10-733-878-411	Sequence 411, App
137	40	50.6	160	3	US-09-833-245-426	Sequence 426, App	210	38	48.1	1388	5	US-10-723-860-2948	Sequence 2948, Ap
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139	40	50.6	302	3	US-09-738-626-6862	Sequence 6862, Ap	212	37	46.8	57	4	US-10-425-115-196590	Sequence 196590,
140	40	50.6	401	4	US-10-108-260A-3987	Sequence 3987, Ap	213	37	46.8	88	4	US-10-425-115-257192	Sequence 257192,
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142	40	50.6	835	4	US-10-437-963-135715	Sequence 135715, A	215	37	46.8	83	4	US-10-425-115-185388	Sequence 185388,
143	40	50.6	916	4	US-10-287-226-330	Sequence 330, App	216	37	46.8	85	4	US-10-767-701-56670	Sequence 56670, A
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145	40	50.6	1142	4	US-10-369-493-1700	Sequence 1700, Ap	218	37	46.8	101	4	US-10-425-115-217780	Sequence 217780,
146	40	50.6	1142	4	US-10-618-581-10	Sequence 10, Appl	219	37	46.8	107	4	US-10-425-115-253127	Sequence 253127,
147	40	50.6	1248	4	US-10-437-963-169178	Sequence 169178, A	220	37	46.8	137	4	US-10-062-467A-3	Sequence 3, Appli
148	39	49.4	157	4	US-10-424-599-195574	Sequence 195574, A	221	37	46.8	159	3	US-08-431-322-26	Sequence 26, Appl
149	39	49.4	225	4	US-10-158-160A-13	Sequence 13, Appl	222	37	46.8	159	4	US-10-372-614-26	Sequence 26, Appl
150	39	49.4	292	4	US-10-158-160A-11	Sequence 11, Appl	223	37	46.8	159	4	US-10-374-603-26	Sequence 26, Appl
151	39	49.4	451	4	US-10-282-122A-47340	Sequence 47340, A	224	37	46.8	159	5	US-10-958-062-26	Sequence 26, Appl
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155	39	49.4	885	4	US-10-156-239-47	Sequence 47, Appl	228	37	46.8	240	4	US-10-437-963-152398	Sequence 152398,
156	39	49.4	887	5	US-10-739-930-10838	Sequence 10838, A	229	37	46.8	260	4	US-10-425-115-195040	Sequence 195040,
157	39	49.4	922	4	US-10-437-963-125036	Sequence 125036, A	230	37	46.8	297	4	US-10-425-115-283055	Sequence 283055,
158	39	49.4	928	4	US-10-080-608A-23	Sequence 23, Appl	231	37	46.8	329	4	US-10-311-642-4	Sequence 4, Appli
159	39	49.4	928	4	US-10-370-685-112	Sequence 112, App	232	37	46.8	405	4	US-10-369-493-3789	Sequence 3789, Ap
160	39	49.4	932	4	US-10-369-493-6025	Sequence 6025, Ap	233	37	46.8	427	4	US-10-425-115-27547	Sequence 27547, A
161	39	49.4	1038	4	US-10-369-493-1708	Sequence 1708, Ap	234	37	46.8	431	4	US-10-182-243-48	Sequence 48, Appl
162	38	48.7	297	5	US-10-450-763-51623	Sequence 51623, A	235	37	46.8	445	4	US-10-282-122A-49547	Sequence 49547, A
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165	38	48.1	87	4	US-10-425-115-205098	Sequence 205098, A	238	37	46.8	528	4	US-10-173-999-103	Sequence 103, App
166	38	48.1	114	4	US-10-437-963-187430	Sequence 187430, A	239	37	46.8	539	4	US-10-156-761-11731	Sequence 11731, A
167	38	48.1	114	4	US-10-425-115-236961	Sequence 236961, A	240	37	46.8	545	4	US-10-029-386-33143	Sequence 33143, A
168	38	48.1	157	4	US-10-424-599-201597	Sequence 201597, A	241	37	46.8	602	4	US-10-369-493-23667	Sequence 23667, A
169	38	48.1	166	3	US-09-764-864-1153	Sequence 1153, Ap	242	37	46.8	627	4	US-10-025-145A-32	Sequence 32, Appl
170	38	48.1	168	4	US-10-437-963-158837	Sequence 158837, A	243	37	46.8	729	6	US-11-097-143-5292	Sequence 5292, Ap
171	38	48.1	176	4	US-10-424-599-175098	Sequence 175098, A	244	37	46.8	811	4	US-10-144-194A-26	Sequence 26, Appl
172	38	48.1	187	4	US-10-437-963-190040	Sequence 190040, A	245	37	46.8	811	4	US-10-144-194A-98	Sequence 98, Appl
173	38	48.1	190	4	US-10-158-160A-16	Sequence 16, Appl	246	37	46.8	811	5	US-10-431-566-26	Sequence 26, Appl

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248	37	46.8	839	4	US-10-437-963-186497	Sequence 186497,	321	36	45.6	673	5	US-10-751-736-106	Sequence 106, App
249	37	46.8	850	4	US-10-437-963-186016	Sequence 186016,	322	36	45.6	695	4	US-10-437-963-176889	Sequence 176889,
250	37	46.8	884	4	US-10-250-889-79	Sequence 79, Appl	323	36	45.6	696	4	US-10-408-765A-1067	Sequence 1067, Ap
251	37	46.8	890	4	US-10-171-311-136	Sequence 196, App	324	36	45.6	702	4	US-10-425-115-223635	Sequence 223635, A
252	37	46.8	890	5	US-10-733-878-459	Sequence 459, App	325	36	45.6	749	4	US-10-425-114-70823	Sequence 70823, A
253	37	46.8	890	5	US-10-737-450-14	Sequence 14, Appl	326	36	45.6	757	4	US-10-220-120-366	Sequence 366, App
254	37	46.8	923	4	US-10-437-963-182305	Sequence 182305,	327	36	45.6	757	4	US-10-363-829-316	Sequence 316, App
255	37	46.8	960	3	US-09-734-426-1	Sequence 1, Appl	328	36	45.6	782	4	US-10-276-774-1718	Sequence 1718, Ap
256	37	46.8	960	4	US-10-264-885-1	Sequence 1, Appl	329	36	45.6	794	4	US-10-425-115-285510	Sequence 285510,
257	37	46.8	993	5	US-10-723-860-1832	Sequence 1832, Ap	330	36	45.6	803	5	US-10-840-060-143	Sequence 143, App
258	37	46.8	1016	4	US-10-753-901-16	Sequence 16, Appl	331	36	45.6	803	6	US-11-097-143-1104	Sequence 1104, Ap
259	37	46.8	1016	4	US-10-754-115-16	Sequence 16, Appl	332	36	45.6	888	4	US-10-425-115-251250	Sequence 251250, A
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262	37	46.8	1274	6	US-11-097-143-24135	Sequence 24135, A	335	36	45.6	1004	4	US-10-437-963-195502	Sequence 195502,
263	37	46.8	1374	6	US-11-018-067-1	Sequence 1, Appl	336	36	45.6	1175	4	US-10-694-711-8	Sequence 8, Appl
264	37	46.8	1437	4	US-10-437-963-189430	Sequence 189430,	337	36	45.6	1224	4	US-10-424-599-251293	Sequence 251293,
265	37	46.8	1500	6	US-11-097-143-17937	Sequence 17937, A	338	36	45.6	1264	4	US-10-032-585-7118	Sequence 7118, Ap
266	37	46.8	1830	4	US-10-437-963-189860	Sequence 189860,	339	36	45.6	1271	4	US-10-437-963-103408	Sequence 103408,
267	37	46.8	3138	6	US-11-097-143-12666	Sequence 12666, A	340	36	45.6	1362	4	US-10-296-838-2	Sequence 2, Appl
268	36.5	46.2	247	5	US-10-450-763-53521	Sequence 53521, A	341	36	45.6	1826	4	US-10-408-765A-1477	Sequence 1477, Ap
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271	36	45.6	72	3	US-09-864-761-40597	Sequence 40597, A	344	35	44.3	89	4	US-10-437-963-156049	Sequence 156049,
272	36	45.6	74	4	US-10-424-599-279780	Sequence 279780,	345	35	44.3	89	4	US-10-424-599-251563	Sequence 251563,
273	36	45.6	75	4	US-10-424-599-150984	Sequence 150984,	346	35	44.3	108	4	US-10-425-115-262998	Sequence 262998,
274	36	45.6	77	4	US-10-156-761-8517	Sequence 8517, Ap	347	35	44.3	114	4	US-10-424-599-215715	Sequence 215715,
275	36	45.6	79	4	US-10-724-972A-4061	Sequence 4061, Ap	348	35	44.3	117	5	US-10-450-763-50902	Sequence 50902, A
276	36	45.6	88	4	US-10-424-599-246121	Sequence 246121,	349	35	44.3	122	4	US-10-238-075-1540	Sequence 1540, Ap
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278	36	45.6	159	4	US-10-437-963-186465	Sequence 186465,	351	35	44.3	137	4	US-10-101-464A-669	Sequence 669, App
279	36	45.6	161	4	US-10-767-701-32708	Sequence 32708, A	352	35	44.3	137	5	US-10-864-252-669	Sequence 669, App
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285	36	45.6	248	3	US-09-804-980-60	Sequence 60, Appl	358	35	44.3	168	4	US-10-369-493-18405	Sequence 18405, A
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290	36	45.6	299	4	US-10-282-122A-50463	Sequence 50463, A	363	35	44.3	194	3	US-09-969-730-341	Sequence 341, App
291	36	45.6	312	4	US-10-424-599-260604	Sequence 260604,	364	35	44.3	194	4	US-10-621-363-341	Sequence 341, App
292	36	45.6	313	5	US-10-732-923-1441	Sequence 1441, Ap	365	35	44.3	198	4	US-10-437-963-181203	Sequence 181203,
293	36	45.6	317	4	US-10-144-156-12	Sequence 12, Appl	366	35	44.3	203	4	US-10-424-599-182148	Sequence 182148,
294	36	45.6	321	4	US-10-238-075-1147	Sequence 1147, Ap	367	35	44.3	221	4	US-10-424-599-232532	Sequence 232532,
295	36	45.6	352	4	US-10-296-838-4	Sequence 4, Appl	368	35	44.3	237	5	US-10-450-763-31586	Sequence 31586, A
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299	36	45.6	384	4	US-10-291-337-2	Sequence 2, Appl	372	35	44.3	294	5	US-10-739-930-8910	Sequence 8910, Ap
300	36	45.6	401	4	US-10-080-170-182	Sequence 182, App	373	35	44.3	296	4	US-10-478-758-8	Sequence 8, Appl
301	36	45.6	401	4	US-10-080-170-182	Sequence 182, App	374	35	44.3	299	4	US-10-437-963-134586	Sequence 134586,
302	36	45.6	401	4	US-10-468-356-182	Sequence 182, App	375	35	44.3	306	3	US-09-726-643-73	Sequence 73, Appl
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304	36	45.6	421	6	US-11-097-143-38148	Sequence 38148, A	377	35	44.3	306	5	US-10-919-272-73	Sequence 73, Appl
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313	36	45.6	581	5	US-10-739-736-3	Sequence 3, Appl	386	35	44.3	340	4	US-10-191-698-1	Sequence 1, Appl
314	36	45.6	583	4	US-10-282-122A-77634	Sequence 77634, A	387	35	44.3	340	4	US-10-420-529-5	Sequence 5, Appl
315	36	45.6	587	6	US-10-437-963-194304	Sequence 194304,	388	35	44.3	340	4	US-10-420-529-20	Sequence 20, Appl
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317	36	45.6	666	4	US-10-425-114-54408	Sequence 54408, A	390	35	44.3	340	4	US-10-608-516-1	Sequence 1, Appl
318	36	45.6	667	4	US-10-425-114-69034	Sequence 69034, A	391	35	44.3	340	5	US-10-861-108-1	Sequence 1, Appl
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394	35	44.3	389	4	US-10-437-963-191059	Sequence 191059, A	467	35	44.3	632	3	US-09-990-443-219	Sequence 219, App
395	35	44.3	394	3	US-09-833-245-1498	Sequence 1498, Ap	468	35	44.3	632	3	US-09-991-854-219	Sequence 219, App
396	35	44.3	395	4	US-10-108-260A-4617	Sequence 4617, Ap	469	35	44.3	632	3	US-09-997-628-219	Sequence 219, App
397	35	44.3	407	5	US-10-128-558-369	Sequence 369, App	470	35	44.3	632	3	US-09-997-683-219	Sequence 219, App
398	35	44.3	408	4	US-10-377-636-2	Sequence 2, Appl	471	35	44.3	632	3	US-09-989-729A-219	Sequence 219, App
399	35	44.3	412	3	US-09-854-731-21	Sequence 21, Appl	472	35	44.3	632	3	US-09-997-349-219	Sequence 219, App
400	35	44.3	414	4	US-10-425-114-40798	Sequence 40798, A	473	35	44.3	632	3	US-09-997-440-219	Sequence 219, App
401	35	44.3	419	3	US-09-726-643-50	Sequence 50, Appl	474	35	44.3	632	3	US-09-990-440-219	Sequence 219, App
402	35	44.3	419	4	US-10-042-141-50	Sequence 50, Appl	475	35	44.3	632	3	US-09-997-857-219	Sequence 219, App
403	35	44.3	419	5	US-10-918-272-50	Sequence 50, Appl	476	35	44.3	632	3	US-09-993-469-219	Sequence 219, App
404	35	44.3	422	5	US-10-739-930-7796	Sequence 7796, Ap	477	35	44.3	632	3	US-09-997-542-219	Sequence 219, App
405	35	44.3	439	4	US-10-108-260A-3726	Sequence 3726, Ap	478	35	44.3	632	3	US-09-993-748-219	Sequence 219, App
406	35	44.3	444	4	US-10-425-114-54918	Sequence 54918, A	479	35	44.3	632	3	US-09-990-439-219	Sequence 219, App
407	35	44.3	447	4	US-10-424-599-276447	Sequence 276447, A	480	35	44.3	632	3	US-09-990-427-219	Sequence 219, App
408	35	44.3	450	4	US-10-425-114-55292	Sequence 55292, A	481	35	44.3	632	3	US-09-989-328-219	Sequence 219, App
409	35	44.3	468	4	US-10-467-535-3	Sequence 3, Appl	482	35	44.3	632	3	US-09-993-583-219	Sequence 219, App
410	35	44.3	471	4	US-10-424-599-266578	Sequence 266578, A	483	35	44.3	632	3	US-09-941-992-219	Sequence 219, App
411	35	44.3	481	4	US-10-425-114-43080	Sequence 43080, A	484	35	44.3	632	3	US-09-992-521-219	Sequence 219, App
412	35	44.3	489	4	US-10-424-599-206716	Sequence 206716, A	485	35	44.3	632	3	US-09-997-333-219	Sequence 219, App
413	35	44.3	506	5	US-10-343-903-17	Sequence 17, Appl	486	35	44.3	632	3	US-09-997-384-219	Sequence 219, App
414	35	44.3	542	4	US-10-425-114-68236	Sequence 68236, A	487	35	44.3	632	3	US-09-998-041-219	Sequence 219, App
415	35	44.3	542	4	US-10-425-115-306619	Sequence 306619, A	488	35	44.3	632	3	US-09-997-585-219	Sequence 219, App
416	35	44.3	549	4	US-10-425-114-64633	Sequence 64633, A	489	35	44.3	632	3	US-09-989-862-219	Sequence 219, App
417	35	44.3	550	5	US-10-450-763-47076	Sequence 47076, A	490	35	44.3	632	3	US-09-997-529-219	Sequence 219, App
418	35	44.3	554	4	US-10-408-765A-2951	Sequence 2951, Ap	491	35	44.3	632	3	US-09-989-725-219	Sequence 219, App
419	35	44.3	562	4	US-10-369-493-10182	Sequence 10182, A	492	35	44.3	632	3	US-09-991-150-219	Sequence 219, App
420	35	44.3	563	4	US-10-369-493-975	Sequence 975, App	493	35	44.3	632	3	US-09-997-641-219	Sequence 219, App
421	35	44.3	571	4	US-10-369-493-39	Sequence 39, Appl	494	35	44.3	632	3	US-09-989-733-219	Sequence 219, App
422	35	44.3	574	4	US-10-425-115-360622	Sequence 360622, A	495	35	44.3	632	3	US-09-992-643-219	Sequence 219, App
423	35	44.3	578	4	US-10-425-115-200250	Sequence 200250, A	496	35	44.3	632	4	US-10-006-867-40	Sequence 40, Appl
424	35	44.3	628	6	US-11-097-143-13773	Sequence 13773, A	497	35	44.3	632	4	US-10-052-586-166	Sequence 166, App
425	35	44.3	631	5	US-10-501-282-1256	Sequence 1256, Ap	498	35	44.3	632	4	US-10-063-547-40	Sequence 40, Appl
426	35	44.3	632	3	US-09-989-722-219	Sequence 219, App	499	35	44.3	632	4	US-10-063-551-40	Sequence 40, Appl
427	35	44.3	632	3	US-09-989-723-219	Sequence 219, App	500	35	44.3	632	4	US-10-174-590-166	Sequence 166, App
428	35	44.3	632	3	US-09-989-727-219	Sequence 219, App	501	35	44.3	632	4	US-10-176-758-166	Sequence 166, App
429	35	44.3	632	3	US-09-989-727-219	Sequence 219, App	502	35	44.3	632	4	US-10-175-737-166	Sequence 166, App
430	35	44.3	632	3	US-09-989-731-219	Sequence 219, App	503	35	44.3	632	4	US-10-063-616-40	Sequence 40, Appl
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432	35	44.3	632	3	US-09-991-073-219	Sequence 219, App	505	35	44.3	632	4	US-10-176-483-166	Sequence 166, App
433	35	44.3	632	3	US-09-990-442-219	Sequence 219, App	506	35	44.3	632	4	US-10-176-749-166	Sequence 166, App
434	35	44.3	632	3	US-09-991-163-219	Sequence 219, App	507	35	44.3	632	4	US-10-176-914-166	Sequence 166, App
435	35	44.3	632	3	US-09-993-604-219	Sequence 219, App	508	35	44.3	632	4	US-10-176-915-166	Sequence 166, App
436	35	44.3	632	3	US-09-990-456-219	Sequence 219, App	509	35	44.3	632	4	US-10-063-569-40	Sequence 40, Appl
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438	35	44.3	632	3	US-09-992-598-219	Sequence 219, App	511	35	44.3	632	4	US-10-063-515-40	Sequence 40, Appl
439	35	44.3	632	3	US-09-989-293A-219	Sequence 219, App	512	35	44.3	632	4	US-10-063-512-40	Sequence 40, Appl
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441	35	44.3	632	3	US-09-990-444-219	Sequence 219, App	514	35	44.3	632	4	US-10-175-738-166	Sequence 166, App
442	35	44.3	632	3	US-09-991-181-219	Sequence 219, App	515	35	44.3	632	4	US-10-175-752-166	Sequence 166, App
443	35	44.3	632	3	US-09-989-730-219	Sequence 219, App	516	35	44.3	632	4	US-10-176-482-166	Sequence 166, App
444	35	44.3	632	3	US-09-990-436-219	Sequence 219, App	517	35	44.3	632	4	US-10-176-757-166	Sequence 166, App
445	35	44.3	632	3	US-09-993-687-219	Sequence 219, App	518	35	44.3	632	4	US-10-176-913-166	Sequence 166, App
446	35	44.3	632	3	US-09-989-734-219	Sequence 219, App	519	35	44.3	632	4	US-10-180-552-166	Sequence 166, App
447	35	44.3	632	3	US-09-997-653-219	Sequence 219, App	520	35	44.3	632	4	US-10-180-557-166	Sequence 166, App
448	35	44.3	632	3	US-09-989-724-219	Sequence 219, App	521	35	44.3	632	4	US-10-063-502-40	Sequence 40, Appl
449	35	44.3	632	3	US-09-989-728-219	Sequence 219, App	522	35	44.3	632	4	US-10-173-700-166	Sequence 166, App
450	35	44.3	632	3	US-09-990-441-219	Sequence 219, App	523	35	44.3	632	4	US-10-174-572-166	Sequence 166, App
451	35	44.3	632	3	US-09-993-667-219	Sequence 219, App	524	35	44.3	632	4	US-10-174-579-166	Sequence 166, App
452	35	44.3	632	3	US-09-997-428-219	Sequence 219, App	525	35	44.3	632	4	US-10-174-582-166	Sequence 166, App
453	35	44.3	632	3	US-09-997-666-219	Sequence 219, App	526	35	44.3	632	4	US-10-175-739-166	Sequence 166, App
454	35	44.3	632	3	US-09-990-438-219	Sequence 219, App	527	35	44.3	632	4	US-10-175-740-166	Sequence 166, App
455	35	44.3	632	3	US-09-990-562-219	Sequence 219, App	528	35	44.3	632	4	US-10-175-743-166	Sequence 166, App
456	35	44.3	632	3	US-09-990-711-219	Sequence 219, App	529	35	44.3	632	4	US-10-175-743-166	Sequence 166, App
457	35	44.3	632	3	US-09-989-726-219	Sequence 219, App	530	35	44.3	632	4	US-10-176-488-166	Sequence 166, App
458	35	44.3	632	3	US-09-998-156-219	Sequence 219, App	531	35	44.3	632	4	US-10-176-492-166	Sequence 166, App
459	35	44.3	632	3	US-09-990-437-219	Sequence 219, App	532	35	44.3	632	4	US-10-176-747-166	Sequence 166, App
460	35	44.3	632	3	US-09-991-157-219	Sequence 219, App	533	35	44.3	632	4	US-10-176-750-166	Sequence 166, App
461	35	44.3	632	3	US-09-997-514-219	Sequence 219, App	534	35	44.3	632	4	US-10-176-985-166	Sequence 166, App
462	35	44.3	632	3	US-09-997-573-219	Sequence 219, App	535	35	44.3	632	4	US-10-176-987-166	Sequence 166, App
463	35	44.3	632	3	US-09-991-172-219	Sequence 219, App	536	35	44.3	632	4	US-10-176-992-166	Sequence 166, App
464	35	44.3	632	3	US-09-990-726-219	Sequence 219, App	537	35	44.3	632	4	US-10-176-993-166	Sequence 166, App
465	35	44.3	632	3	US-09-997-559-219	Sequence 219, App	538	35	44.3	632	4	US-10-176-993-166	Sequence 166, App

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686	35	44.3	632	4	US-10-192-015-166	Sequence 166, App	759	35	44.3	632	4	US-10-205-902-166	Sequence 166, App
687	35	44.3	632	4	US-10-194-394-166	Sequence 166, App	760	35	44.3	632	4	US-10-205-907-166	Sequence 166, App
688	35	44.3	632	4	US-10-194-425-166	Sequence 166, App	761	35	44.3	632	4	US-10-176-484-166	Sequence 166, App
689	35	44.3	632	4	US-10-194-485-166	Sequence 166, App	762	35	44.3	632	4	US-10-194-456-166	Sequence 166, App
690	35	44.3	632	4	US-10-195-885-166	Sequence 166, App	763	35	44.3	632	4	US-10-196-758-166	Sequence 166, App
691	35	44.3	632	4	US-10-195-899-166	Sequence 166, App	764	35	44.3	632	4	US-10-198-770-166	Sequence 166, App
692	35	44.3	632	4	US-10-196-748-166	Sequence 166, App	765	35	44.3	632	4	US-10-199-308-166	Sequence 166, App
693	35	44.3	632	4	US-10-196-750-166	Sequence 166, App	766	35	44.3	632	4	US-10-200-617-166	Sequence 166, App
694	35	44.3	632	4	US-10-197-699-166	Sequence 166, App	767	35	44.3	632	4	US-10-205-893-166	Sequence 166, App
695	35	44.3	632	4	US-10-197-700-166	Sequence 166, App	768	35	44.3	632	4	US-10-205-897-166	Sequence 166, App
696	35	44.3	632	4	US-10-197-705-166	Sequence 166, App	769	35	44.3	632	4	US-10-063-563-40	Sequence 40, Appl
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ALIGNMENTS

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; Sequence 4, Application US/10517510
; Publication No. US20050164201A1
; GENERAL INFORMATION:
; APPLICANT: Harvey, Diane Marie
; APPLICANT: Yang, Yi
; APPLICANT: Kohl, Nancy
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
US-10-517-510-4
Query Match 100.0%; Score 79; DB 5; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203

RESULT 2
US-10-517-510-2
; Sequence 2, Application US/10517510
; Publication No. US20050164201A1
; GENERAL INFORMATION:
; APPLICANT: Harvey, Diane Marie
; APPLICANT: Yang, Yi
; APPLICANT: Kohl, Nancy
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
US-10-517-510-2
Query Match 100.0%; Score 79; DB 5; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203

RESULT 3
US-10-828-985A-11
; Sequence 11, Application US/10828985A
; Publication No. US20050003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Engle, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoremas, Nicholas F
; TITLE OF INVENTION: Novel Isoforms of Centromere Protein E (CENPE)
; FILE REFERENCE: RS0210Y
; CURRENT APPLICATION NUMBER: US/10/828,985A
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US 60/464,905
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/510,701
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 2503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-828-985A-11
Query Match 100.0%; Score 79; DB 5; Length 2503;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203

RESULT 4
US-10-828-985A-9
; Sequence 9, Application US/10828985A
; Publication No. US20050003402A1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Castle, John C
; APPLICANT: Garrett-Engle, Philip W
; APPLICANT: Kan, Zhengyan
; APPLICANT: Loerch, Patrick M
; APPLICANT: Tsinoremas, Nicholas F
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: A NOVEL CENTROMERE-ASSOCIATED MOTOR PROTEIN, AND USES
; FILE REFERENCE: 21023P
; CURRENT APPLICATION NUMBER: US/10/517,510
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/18203
; PRIOR FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: 60/387,403
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Human
US-10-517-510-2
Query Match 100.0%; Score 79; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
Db 189 RHYGETKNQSRSS 203
```

: PRIOR APPLICATION NUMBER: 09/540,217

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, PRIOR APPLICATION NUMBER: 09/340,421
, PRIOR FILING DATE: 2000-03-31
, PRIOR APPLICATION NUMBER: 09/649,167
, PRIOR FILING DATE: 2000-03-31
, PRIOR APPLICATION NUMBER: 09/649,167
, PRIOR FILING DATE: 2000-03-31
, PRIOR FILING DATE: 2000-08-23
, NUMBER OF SEQ ID NOS: 60736
, SOFTWARE: CuiTom
, SEQ ID NO 36864
, LENGTH: 2633
, TYPE: PRT
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: DOMAIN
, LOCATION: (77)..(99)
, OTHER INFORMATION: KINSIN HEAVY CHAIN
, OTHER INFORMATION: accession number
, FEATURE:
, NAME/KEY: DOMAIN
, LOCATION: (12)..(2412)
, OTHER INFORMATION: Kinsin motor domain
, OTHER INFORMATION: kinsin, E-value
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (1)..(2633)
, OTHER INFORMATION: Xaa = X or * as
US-10-450-763-36964

```

```

? FEATURE:
? NAME/KEY: DOMAIN
? LOCATION: (12) ..(2412)
? OTHER INFORMATION: Kinesin motor domain identified by Pfam, accession name
? :
? OTHER INFORMATION: kinesin. E-value=4.9e-217. Pfam score of 734.4
? :

```

```

; OTHER INFORMATION: KLINEBELL,
;
; FEATURE:
;
; NAME/KEY: misc_feature
;
; LOCATION: (1)...(2633)
;
; OTHER INFORMATION: Xaa = X o
US-10-450-763-36864

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```

Query Match          100.0%; Score
Best Local Similarity 100.0%; Pred
Matches 15; Conservative 0; Mi
                                0
QY      1 RHYGETKMNQRSSRS 15
      |||||
Db      189 RHYGETKMNQRSSRS 203
      |||||

RESULT 7
US-10-723-860-749
; Sequence 749, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagn
; TITLE OF INVENTION: Methods for Scr
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/72
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,73
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 749
; LENGTH: 2663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-749

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```

; SOFTWARE: FACULTIN VERSION 3.2
; SEQ ID NO 749
; LENGTH: 2663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-749

```

US-10-723-860-749

QY	1	RHYGETKQNRSSRS	15
Db	189	RHYGETKQNRSSRS	203

RESULT 8
 US-10-650-280-1
 ; Sequence 1, Application US/106503080
 ; Publication NO. US20050191631A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, Kenneth W.

APPLICANT: Sakowicz, Roman
APPLICANT: Goldstein, Lawrence S.B.
APPLICANT: Cleveland, Don W.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
FILE REFERENCE: 18557C-000110US
CURRENT APPLICATION NUMBER: US/10/650,280
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/150,867
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,645
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2954
TYPE: PRT
ORGANISM: Xenopus sp.
FEATURE:
OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
OTHER INFORMATION: member of the kinesin superfamily of microtubule
OTHER INFORMATION: motor proteins
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(472)
OTHER INFORMATION: kinesin like motor domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (473)..(2752)
OTHER INFORMATION: rod domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (2753)..(2954)
OTHER INFORMATION: tail domain
US-10-650-280-1

Query Match 87.3%; Score 69; DB 5; Length 2954;
Best Local Similarity 86.7%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 187 RHYGETKNQRRSRS 201

RESULT 9
US-10-425-115-263022
Sequence 263022, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 263022
LENGTH: 668
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_171488C.1.pep
US-10-425-115-263022

Query Match 82.3%; Score 65; DB 4; Length 668;
Best Local Similarity 80.0%; Pred. No. 0.0086;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 195 RHYGETKNQRRSRS 209
RESULT 10
US-10-425-114-59725
Sequence 59725, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59725
LENGTH: 694
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3912-011-C4_FLI.pep
US-10-425-114-59725

Query Match 82.3%; Score 65; DB 4; Length 694;
Best Local Similarity 80.0%; Pred. No. 0.0089;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 221 RHYGETKNQRRSRS 235

RESULT 11
US-10-437-963-116808
Sequence 116808, Application US/10437963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 116808
LENGTH: 201
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_20274C.1.pep
US-10-437-963-116808

Query Match 79.7%; Score 63; DB 4; Length 201;
Best Local Similarity 80.0%; Pred. No. 0.0054;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 41 RHYGETKNQRRSRS 55


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Query Match      65.8%; Score 52; DB 3; Length 154;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHVGETKNQRRSRS 15
      |||..|||..|||
DB      29 RHGTGTQNEHSRS 43

RESULT 14
US-10-437-963-176714
; Sequence 176714, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176714
; LENGTH: 1382
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_74437C.1.pep
US-10-437-963-176714

Query Match      65.8%; Score 52; DB 4; Length 1382;
Best Local Similarity 73.3%; Pred. No. 3.9;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHVGETKNQRRSRS 15
      |||..|||..|||
DB      180 RHIGETNMNVSSRS 194

RESULT 15
US-10-287-226-142
; Sequence 142, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.
; APPLICANT: Miller, Charles B.,
; APPLICANT: Millet, Isabelle,

```

```
/ APPLICANT: Ooi, Chean Eng,
/ APPLICANT: Ort, Tatiana,
/ APPLICANT: Padigaru, Muralidhara,
/ APPLICANT: Patturajan, Meera,
/ APPLICANT: Rastelli, Luca,
/ APPLICANT: Rieger, Daniel K.,
/ APPLICANT: Rothenberg, Mark B.,
/ APPLICANT: Shenoy, Suresh G.,
/ APPLICANT: Spaderna, Steven K.,
/ APPLICANT: Spytek, Kimberley A.,
/ APPLICANT: Taupier, Jr., Raymond J.,
/ APPLICANT: Vernet, Corine A.M.,
/ APPLICANT: Zerhusen, Bryan D.,
/ APPLICANT: Zhong, Mei
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/
/ FILE REFERENCE: 21402-480C
/ CURRENT APPLICATION NUMBER: US/10/287,226
/ CURRENT FILING DATE: 2002-11-04
/ PRIOR APPLICATION NUMBER: 60/334,421
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,392
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/360,148
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: 60/364,000
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/404,821
/ PRIOR FILING DATE: 2002-08-20
/ PRIOR APPLICATION NUMBER: 60/334,526
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 60/354,409
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 60/364,227
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/334,027
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/331,641
/ PRIOR FILING DATE: 2001-11-20
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 673
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO 142
/ LENGTH: 1401
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-226-142

Query Match 65.8%; Score 52; DB 4; Length 1401;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNRSRS 15
Db 193 RHTGTQNEHSRS 207

RESULT 16
US-11-097-143-9828
/ Sequence 9828, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/
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/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9828
/ LENGTH: 1931
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-9828

Query Match 65.8%; Score 52; DB 6; Length 1931;
Best Local Similarity 73.3%; Pred. No. 5.5;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNRSRS 15
Db 183 RVGGETNNRSRS 197

RESULT 17
US-10-425-115-245875
/ Sequence 245875, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kowalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 245875
/ LENGTH: 197
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_155820C.1.pep
US-10-425-115-245875

Query Match 64.6%; Score 51; DB 4; Length 197;
Best Local Similarity 73.3%; Pred. No. 0.73;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNRSRS 15
Db 167 RHIGETDNNLYSRS 181

RESULT 18
US-11-097-143-22341
/ Sequence 22341, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/
```

RESULT 20
US-10-797-893-6
; Section 6, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor pr

```

RESULT 22
US-09-925-300-1228
; Sequence 1228, Application US/09925300
; Patent No. US20020151681A1
;
GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
;

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1228
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (75)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (435)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1228
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Query Match          62.0%; Score 49; DB 3; Length 460;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 1 RHYGETKNQSRSS 15
    | | | | | | | |
Db 210 RTVGATRLNQSRSS 224
```

```
RESULT 23
US-10-797-893-8
; Sequence 8, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-10-797-893-8
```

```
Query Match          62.0%; Score 49; DB 4; Length 487;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 RHYGETKNQSRSS 15
    | | | | | | | |
Db 208 RTVGATRLNQSRSS 222
```

```
RESULT 24
US-10-334-143-80
; Sequence 80, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SVACHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-80
```

```
Query Match          62.0%; Score 49; DB 4; Length 490;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 RHYGETKNQSRSS 15
    | | | | | | | |
Db 240 RTVGATRLNQSRSS 254
```

```
RESULT 25
US-10-797-893-4
; Sequence 4, Application US/10797893
; Publication No. US20040142397A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Novel motor proteins and methods for
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1044
; CURRENT APPLICATION NUMBER: US/10/797,893
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: US/09/724,224
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/597,292
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Human
US-10-797-893-4
```

```
Query Match          62.0%; Score 49; DB 4; Length 512;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 RHYGETKNQSRSS 15
    | | | | | | | |
Db 233 RTVGATRLNQSRSS 247
```

```
RESULT 26
US-10-733-878-425
; Sequence 425, Application US/10733878
; Publication No. US20040224408A1
; GENERAL INFORMATION:
; APPLICANT: Jean-Philippe Girard
; APPLICANT: Francois Amalric
; APPLICANT: Myriam Roussigne
; APPLICANT: Thomas Clouaire
; TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
; TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
; TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
; FILE REFERENCE: BIOBANK.012A
; CURRENT APPLICATION NUMBER: US/10/733,878
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432699
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/485027
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-733-878-425

Query Match 62.0%; Score 49; DB 5; Length 665;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
DB 232 RTVGATRLNQSRSS 246

RESULT 27

US-09-874-923-53

; Sequence 53, Application US/09874923

; Patent No. US20020081320A1

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Webb, John R.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Skeiky, Yaseir A.W.

; APPLICANT: Bhatia, Ajay

; APPLICANT: Coler, Rhea

; APPLICANT: Probst, Peter

; APPLICANT: Brannon, Mark

; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

; FILE REFERENCE: 210121.420C8

; CURRENT APPLICATION NUMBER: US/09/874,923

; CURRENT FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53

; LENGTH: 324

; TYPE: PRT

; ORGANISM: Leishmania chagasi

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(324)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-874-923-53

Query Match 60.8%; Score 48; DB 3; Length 324;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
DB 234 RHTAATKFNDRSSRS 248

RESULT 28

US-09-991-496-53

; Sequence 53, Application US/09991496

; Patent No. US20020169285A1

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Webb, John R.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Skeiky, Yaseir A.W.

; APPLICANT: Bhatia, Ajay

; APPLICANT: Coler, Rhea

; APPLICANT: Probst, Peter

; APPLICANT: Brannon, Mark

; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE

; FILE REFERENCE: 210121.420C9

; CURRENT APPLICATION NUMBER: US/09/991,496

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53

; LENGTH: 324

; TYPE: PRT

; ORGANISM: Leishmania chagasi

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: 79, 96

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-991-496-53

Query Match 60.8%; Score 48; DB 3; Length 324;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
DB 234 RHTAATKFNDRSSRS 248

RESULT 29

US-10-437-963-114373

; Sequence 114373, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 114373

; LENGTH: 420

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_18070C.1.pep

US-10-437-963-114373

Query Match 60.8%; Score 48; DB 4; Length 420;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMNQSRSS 15
DB 197 RQIGETAMNEASSRS 211

RESULT 30

US-10-437-963-114370

; Sequence 114370, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

```
; SEQ ID NO 114370
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18069C.1.pep
US-10-437-963-114370

Query Match          60.8%; Score 48; DB 4; Length 821;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
    |||||:||||
Db 167 ROIGETANNEASSRS 181

RESULT 31
US-10-437-963-163527
; Sequence 163527, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163527
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62515C.1.pep
US-10-437-963-163527

Query Match          60.8%; Score 48; DB 4; Length 906;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
    |||||:||||
Db 206 RHAANTKNTESSRS 220

RESULT 32
US-09-826-734-144
; Sequence 144, Application US/09826734
; Publication No. US20030017457A1
; GENERAL INFORMATION:
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Mishra, Vishnu S.
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Kekuda, Ramesha
; TITLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-754
; CURRENT APPLICATION NUMBER: US/09/826,734
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,576
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 270
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 114370
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18069C.1.pep
US-10-437-963-114370

Query Match          60.8%; Score 48; DB 4; Length 821;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
    |||||:||||
Db 167 ROIGETANNEASSRS 181

RESULT 31
US-10-437-963-163527
; Sequence 163527, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163527
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62515C.1.pep
US-10-437-963-163527

Query Match          60.8%; Score 48; DB 4; Length 906;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
    |||||:||||
Db 206 RHAANTKNTESSRS 220

RESULT 32
US-09-826-734-144
; Sequence 144, Application US/09826734
; Publication No. US20030017457A1
; GENERAL INFORMATION:
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Mishra, Vishnu S.
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Kekuda, Ramesha
; TITLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-754
; CURRENT APPLICATION NUMBER: US/09/826,734
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,576
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 270
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 144
; LENGTH: 54
; TYPE: PRT
; ORGANISM: homo sapiens
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108604C.1.pep
US-10-424-599-152360

Query Match          59.5%; Score 47; DB 3; Length 54;
Best Local Similarity 64.3%; Pred. No. 0.95;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 HYGETKNQRRSRS 15
    |||||:||||
Db 1 HTGTTQMNHSRS 14

RESULT 33
US-10-424-599-152360
; Sequence 152360, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 152360
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(75)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108604C.1.pep
US-10-424-599-152360

Query Match          59.5%; Score 47; DB 4; Length 75;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
    |||||:||||
Db 2 RSVGKTQNEQSRS 16

RESULT 34
US-10-425-115-201216
; Sequence 201216, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201216
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115095C.1.pep
US-10-425-115-201216
```


US-10-425-115-200354
; Sequence 200354, Application US/10425115
; Publication No. US2004014272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 200354
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(789)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_11430C.1.pap
US-10-425-115-200354

Query Match 59.5%; Score 47; DB 4; Length 789;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |

Db 633 RSVGKTQNEQSSRS 647

RESULT 40
US-10-437-963-173873
; Sequence 173873, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173873
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7186C.1.pap
US-10-437-963-173873

Query Match 58.2%; Score 46; DB 4; Length 762;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |

Db 607 RSVGKTQNEQSSRS 621

RESULT 41
US-10-437-963-173884

; Sequence 173884, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173884
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7187C.1.pap
US-10-437-963-173884

Query Match 58.2%; Score 46; DB 4; Length 788;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |

Db 632 RSVGKTQNEQSSRS 646

RESULT 42
US-10-473-276-1
; Sequence 1, Application US/10473276
; Publication No. US20040158893A1
; GENERAL INFORMATION:
; APPLICANT: Dickinson, Hugh
; APPLICANT: Scott, Roderick
; APPLICANT: Spielman, Melissa
; TITLE OF INVENTION: FINAL SEGREGATION OF MALE MEIOTIC PRODUCTS IN PLANTS
; FILE REFERENCE: 046658/269934
; CURRENT APPLICATION NUMBER: US/10/473,276
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/GB02/01466
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: GB 0108050.6
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-473-276-1

Query Match 58.2%; Score 46; DB 4; Length 932;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQSSRS 15
| | | | |
| | | | |

Db 207 RQVGTALNDKSSRS 221

RESULT 43
US-10-437-963-113879
; Sequence 113879, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.


```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113879
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17625C.1.pep
US-10-437-963-113879

Query Match 57.0%; Score 45; DB 4; Length 114;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
DB 68 RRTGETFLNEKRSRS 82

RESULT 44
US-10-767-701-36255
; Sequence 36255, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 36255
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(252)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C8566_1.pep
US-10-767-701-36255

Query Match 57.0%; Score 45; DB 4; Length 252;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
DB 180 RSVGRTQMNESSRS 194

RESULT 45
US-10-424-599-174384
; Sequence 174384, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
```

```
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174384
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128488C.1.pep
US-10-424-599-174384

Query Match 57.0%; Score 45; DB 4; Length 312;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
DB 103 RQIGETALNEASSRS 117

RESULT 46
US-10-425-114-45648
; Sequence 45648, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45648
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700282006_FLI.pep
US-10-425-114-45648

Query Match 57.0%; Score 45; DB 4; Length 328;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKMQRSRS 15
DB 178 RSVGRTQMNESSRS 192

RESULT 47
US-10-425-115-243578
; Sequence 243578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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; SEQ ID NO 243578
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_153726C.1.pep
US-10-425-115-243578

Query Match      57.0%; Score 45; DB 4; Length 413;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 263 RSVGRQTQMESSRS 277

RESULT 48
US-10-437-963-196324
; Sequence 196324, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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; LENGTH: 515
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92186C.1.pep
US-10-437-963-196324

Query Match      57.0%; Score 45; DB 4; Length 515;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 363 RSVGRQTQMESSRS 377

RESULT 49
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; Sequence 242676, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 242676
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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
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; OTHER INFORMATION: Clone ID: MRT4577_152904C.1.pep
US-10-425-115-242676

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Best Local Similarity 60.0%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 122 RRTGETFLNEKSSRS 136

RESULT 50
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; Sequence 17, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-080-608A-17

Query Match      57.0%; Score 45; DB 4; Length 956;
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Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRRSRS 15
Db 191 RHVAVTNNNEHSSRS 205

Search completed: April 21, 2006, 13:56:58
Job time : 180 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 21, 2006, 13:54:16 ; Search time 26 seconds
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25.386 Million cell updates/sec

Title: US-09-993-399-1

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Scoring table: BLOSUM62

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Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB pep.*
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- 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	51	64.6	743	7	US-11-096-568A-215
5	51	64.6	829	7	US-11-096-568A-215
6	51	64.6	834	7	US-11-096-568A-215
7	51	64.6	851	7	US-11-096-568A-215
8	51	64.6	862	7	US-11-096-568A-215
9	46	58.2	811	7	US-11-096-568A-215
10	46	58.2	898	7	US-11-096-568A-215
11	46	58.2	932	7	US-11-096-568A-215
12	45	57.0	315	7	US-11-051-720-1345
13	45	57.0	324	7	US-11-051-720-1345
14	45	57.0	385	7	US-11-051-720-1345
15	45	57.0	514	7	US-11-051-720-1345
16	45	57.0	737	7	US-11-051-720-1345
17	45	57.0	911	6	US-10-330-773-709
18	45	57.0	952	6	US-10-330-773-709
19	45	57.0	957	7	US-11-051-720-1345
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21	44	55.7	331	7	US-11-096-568A-26778
22	44	55.7	338	7	US-11-096-568A-26777
23	44	55.7	799	7	US-11-096-568A-26771
24	44	55.7	808	7	US-11-096-568A-26770
25	44	55.7	842	7	US-11-096-568A-26770

26	44	55.7	849	7	US-11-096-568A-26769	Sequence 26769, A
27	44	55.7	897	7	US-11-096-568A-26948	Sequence 26948, A
28	43	54.4	975	7	US-11-096-568A-27943	Sequence 27943, A
29	43	54.4	983	7	US-11-096-568A-27942	Sequence 27942, A
30	43	54.4	1039	7	US-11-096-568A-30324	Sequence 30324, A
31	43	54.4	1055	7	US-11-096-568A-30323	Sequence 30323, A
32	43	54.4	1063	7	US-11-096-568A-30322	Sequence 30322, A
33	43	54.4	1087	7	US-11-096-568A-27941	Sequence 27941, A
34	41	51.9	970	7	US-11-096-568A-34153	Sequence 34153, A
35	41	51.9	1035	7	US-11-096-568A-34152	Sequence 34152, A
36	41	51.9	1042	7	US-11-096-568A-34151	Sequence 34151, A
37	40	50.6	302	7	US-11-082-389-84	Sequence 84, Appl
38	40	50.6	1142	7	US-11-079-463-10327	Sequence 3831, Ap
39	38	48.1	453	7	US-11-079-463-10327	Sequence 10327, A
40	38	48.1	506	7	US-11-188-298-19543	Sequence 19543, A
41	37	46.8	290	6	US-10-506-454-292	Sequence 292, App
42	37	46.8	334	7	US-11-098-686-11287	Sequence 11287, A
43	37	46.8	353	7	US-11-098-686-10227	Sequence 10227, A
44	37	46.8	575	7	US-11-087-099-422	Sequence 422, App
45	37	46.8	1145	7	US-11-096-568A-29274	Sequence 29274, A
46	37	46.8	1160	7	US-11-096-568A-29273	Sequence 29273, A
47	37	46.8	1195	7	US-11-096-568A-29272	Sequence 29272, A
48	36	45.6	204	7	US-11-045-004-1154	Sequence 1154, Ap
49	36	45.6	313	7	US-11-188-298-20356	Sequence 20356, A
50	36	45.6	317	7	US-11-152-569-12	Sequence 12, Appl
51	36	45.6	384	7	US-11-187-571-2	Sequence 2, Appl
52	36	45.6	411	7	US-11-188-298-10624	Sequence 10624, A
53	36	45.6	750	7	US-11-096-568A-18049	Sequence 18049, A
54	36	45.6	802	7	US-11-096-568A-18048	Sequence 18048, A
55	36	45.6	823	7	US-11-096-568A-18047	Sequence 18047, A
56	36	45.6	1493	6	US-10-330-773-502	Sequence 502, App
57	36	45.6	1826	6	US-10-330-773-499	Sequence 499, App
58	35	44.3	194	6	US-10-986-501-341	Sequence 341, App
59	35	44.3	340	7	US-11-145-532-5	Sequence 5, Appl
60	35	44.3	340	7	US-11-145-532-21	Sequence 21, Appl
61	35	44.3	389	7	US-11-188-298-16747	Sequence 16747, A
62	35	44.3	391	7	US-11-096-568A-22689	Sequence 22689, A
63	35	44.3	392	7	US-11-188-298-6028	Sequence 6028, Ap
64	35	44.3	411	7	US-11-188-298-18419	Sequence 18419, A
65	35	44.3	412	7	US-11-188-298-11847	Sequence 11847, A
66	35	44.3	440	7	US-11-096-568A-22688	Sequence 22688, A
67	35	44.3	444	7	US-11-096-568A-22687	Sequence 22687, A
68	35	44.3	632	6	US-10-063-703-40	Sequence 40, Appl
69	35	44.3	632	6	US-10-194-487-166	Sequence 166, App
70	35	44.3	632	6	US-10-195-883-166	Sequence 166, App
71	35	44.3	632	6	US-10-195-888-166	Sequence 166, App
72	35	44.3	632	6	US-10-195-888-166	Sequence 166, App
73	35	44.3	632	6	US-11-103-240-40	Sequence 40, Appl
74	35	44.3	632	7	US-11-103-195-40	Sequence 40, Appl
75	35	44.3	660	6	US-10-131-826A-480	Sequence 480, App
76	35	44.3	660	6	US-10-973-115B-480	Sequence 480, App
77	35	44.3	660	6	US-11-290-153-480	Sequence 480, App
78	35	44.3	746	7	US-11-024-959-346	Sequence 346, App
79	35	44.3	746	7	US-11-079-463-8339	Sequence 8339, Ap
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82	34	43.0	214	7	US-11-188-298-9651	Sequence 9651, Ap
83	34	43.0	215	7	US-11-096-568A-20683	Sequence 20683, A
84	34	43.0	202	7	US-11-087-099-1820	Sequence 1820, Ap
85	34	43.0	302	7	US-11-188-298-2559	Sequence 2559, Ap
86	34	43.0	302	7	US-11-188-298-6674	Sequence 6674, Ap
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88	34	43.0	414	7	US-11-096-568A-32139	Sequence 32139, A
89	34	43.0	414	7	US-11-188-298-21422	Sequence 21422, A
90	34	43.0	472	7	US-11-096-568A-32138	Sequence 32138, A
91	34	43.0	472	7	US-11-188-298-6721	Sequence 6721, Ap
92	34	43.0	494	7	US-11-096-568A-32137	Sequence 32137, A
93	34	43.0	498	6	US-10-204-639-37	Sequence 37, Appl
94	34	43.0	542	6	US-10-858-730-106	Sequence 106, App
95	34	43.0	640	7	US-11-087-099-2757	Sequence 2757, Ap
96	34	43.0	798	7	US-11-072-512-3335	Sequence 3335, Ap
97	34	43.0	1267	7	US-11-109-156-35	Sequence 35, Appl
98	34	43.0				

99	34	43.0	1653	6	US-10-453-372-866	Sequence 866, App	172	32	40.5	486	7	US-11-096-568A-28698	Sequence 28698, A
100	34	43.0	2340	7	US-11-052-554A-171	Sequence 171, App	173	32	40.5	494	7	US-11-096-568A-28697	Sequence 28697, A
101	33.5	42.4	131	7	US-11-045-004-2632	Sequence 2632, App	174	32	40.5	500	6	US-10-467-657-3344	Sequence 3344, App
102	33.5	42.4	320	6	US-10-995-561-947	Sequence 947, App	175	32	40.5	515	7	US-11-096-568A-28696	Sequence 28696, A
103	32.5	42.4	372	6	US-10-844-035-1	Sequence 1, Appl	176	32	40.5	534	7	US-11-096-568A-14686	Sequence 14686, A
104	33.5	42.4	373	6	US-10-995-561-948	Sequence 948, App	177	32	40.5	534	7	US-11-096-568A-14686	Sequence 14686, A
105	33.5	42.4	375	6	US-10-995-561-946	Sequence 946, App	178	32	40.5	534	7	US-11-096-568A-32514	Sequence 32514, A
106	33.5	42.4	385	6	US-10-995-561-945	Sequence 945, App	179	32	40.5	567	7	US-11-096-568A-32513	Sequence 32513, A
107	33.5	42.4	385	6	US-10-995-561-949	Sequence 949, App	180	32	40.5	572	7	US-11-052-554A-129	Sequence 129, App
108	33.5	42.4	439	7	US-11-045-004-1683	Sequence 1683, App	181	32	40.5	637	7	US-11-113-837-4	Sequence 4, Appl
109	33	41.8	117	6	US-10-507-662-46	Sequence 46, Appl	182	32	40.5	649	7	US-11-109-157A-7	Sequence 7, Appl
110	33	41.8	110	6	US-11-077-619-76	Sequence 76, Appl	183	32	40.5	714	7	US-11-096-568A-32512	Sequence 32512, A
111	33	41.8	126	6	US-10-507-662-19	Sequence 19, Appl	184	32	40.5	752	7	US-11-094-917-33	Sequence 33, Appl
112	33	41.8	222	7	US-11-096-568A-12051	Sequence 12051, A	185	32	40.5	762	7	US-11-055-822-912	Sequence 912, App
113	33	41.8	244	7	US-11-096-568A-19010	Sequence 19010, A	186	32	40.5	785	7	US-11-052-554A-6	Sequence 6, Appl
114	33	41.8	247	7	US-11-087-099-6223	Sequence 6223, App	187	32	40.5	811	7	US-11-079-453-7729	Sequence 7729, App
115	33	41.8	247	7	US-11-188-298-16722	Sequence 16722, A	188	32	40.5	875	7	US-11-045-004-126	Sequence 126, App
116	33	41.8	249	6	US-10-527-500-25	Sequence 25, Appl	189	32	40.5	887	7	US-11-096-568A-29796	Sequence 29796, A
117	33	41.8	252	7	US-11-098-686-11048	Sequence 11048, A	190	32	40.5	896	7	US-11-188-298-4356	Sequence 4356, App
118	33	41.8	271	7	US-11-096-568A-19009	Sequence 19009, A	191	32	40.5	917	7	US-11-096-568A-29795	Sequence 29795, A
119	33	41.8	330	7	US-11-074-176-174	Sequence 174, App	192	32	40.5	934	7	US-11-108-864-19	Sequence 19, Appl
120	33	41.8	330	7	US-11-087-099-2823	Sequence 2823, App	193	32	40.5	961	7	US-11-096-568A-29794	Sequence 29794, A
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122	33	41.8	338	7	US-11-045-004-862	Sequence 862, App	195	32	40.5	1067	7	US-11-062	Sequence 3, Appl
123	33	41.8	362	7	US-11-096-568A-19008	Sequence 19008, A	196	32	40.5	1070	7	US-11-109-157A-5	Sequence 5, Appl
124	33	41.8	470	7	US-11-186-284-123	Sequence 123, App	197	32	40.5	1076	7	US-11-109-157A-5	Sequence 4, Appl
125	33	41.8	490	7	US-11-188-298-9166	Sequence 9166, App	198	32	40.5	1084	7	US-11-062	Sequence 8, Appl
126	33	41.8	502	7	US-11-188-298-19312	Sequence 19312, A	199	32	40.5	1092	7	US-11-062	Sequence 6, Appl
127	33	41.8	511	7	US-11-045-004-42	Sequence 42, Appl	200	32	40.5	1095	7	US-11-062	Sequence 7, Appl
128	33	41.8	535	6	US-10-131-826A-124	Sequence 124, App	201	32	40.5	1122	6	US-10-330-773-260	Sequence 260, App
129	33	41.8	535	6	US-10-973-115B-124	Sequence 124, App	202	32	40.5	1152	7	US-11-080-026-4	Sequence 4, Appl
130	33	41.8	535	7	US-11-290-153-124	Sequence 124, App	203	32	40.5	1786	7	US-11-188-298-4785	Sequence 4785, App
131	33	41.8	684	7	US-11-079-463-10136	Sequence 10136, A	204	32	40.5	1907	7	US-11-039-398-25	Sequence 25, Appl
132	33	41.8	896	7	US-11-188-298-8754	Sequence 8754, App	205	32	40.5	2556	7	US-11-050-346-67	Sequence 67, Appl
133	33	41.8	906	7	US-11-087-099-11997	Sequence 11997, A	206	31.5	39.9	320	6	US-10-453-372-854	Sequence 854, App
134	33	41.8	922	7	US-11-072-512-2694	Sequence 2694, App	207	31.5	39.9	844	6	US-10-453-372-852	Sequence 852, App
135	33	41.8	934	7	US-11-052-554A-10	Sequence 10, Appl	208	31.5	39.9	844	6	US-10-453-372-856	Sequence 856, App
136	32	40.5	17	6	US-10-507-662-4	Sequence 4, Appl	209	31.5	39.9	938	7	US-10-330-773-873	Sequence 873, App
137	32	40.5	20	7	US-11-188-187A-32	Sequence 32, Appl	210	31	39.2	14	7	US-11-072-512-3855	Sequence 3855, App
138	32	40.5	49	6	US-10-467-657-4194	Sequence 4194, App	211	31	39.2	14	7	US-11-116-144-184	Sequence 184, App
139	32	40.5	126	6	US-10-507-662-21	Sequence 20, Appl	212	31	39.2	59	7	US-11-220-372-184	Sequence 184, App
140	32	40.5	126	6	US-10-507-662-21	Sequence 21, Appl	213	31	39.2	59	6	US-11-096-568A-561	Sequence 561, App
141	32	40.5	130	7	US-11-188-187A-3	Sequence 3, Appl	214	31	39.2	91	6	US-10-485-788A-652	Sequence 652, App
142	32	40.5	222	6	US-10-793-626-376	Sequence 376, App	215	31	39.2	91	7	US-11-053-076-124	Sequence 124, App
143	32	40.5	250	6	US-10-467-657-3132	Sequence 3132, App	216	31	39.2	122	6	US-10-506-454-1174	Sequence 1174, App
144	32	40.5	252	7	US-11-096-568A-1494	Sequence 1494, App	217	31	39.2	148	7	US-11-098-686-101	Sequence 101, App
145	32	40.5	257	7	US-11-096-568A-1493	Sequence 1493, App	218	31	39.2	172	7	US-11-096-568A-4476	Sequence 4476, App
146	32	40.5	264	7	US-11-096-568A-1492	Sequence 1492, App	219	31	39.2	173	7	US-11-096-568A-4475	Sequence 4475, App
147	32	40.5	287	6	US-10-976-016-1	Sequence 1, Appl	220	31	39.2	189	7	US-11-096-568A-34078	Sequence 34078, A
148	32	40.5	308	7	US-11-188-298-3745	Sequence 3745, App	221	31	39.2	202	7	US-11-123-241-50	Sequence 50, Appl
149	32	40.5	308	7	US-11-188-298-10390	Sequence 10390, A	222	31	39.2	208	7	US-11-079-463-7850	Sequence 7850, App
150	32	40.5	315	7	US-11-096-568A-20497	Sequence 20497, A	223	31	39.2	215	7	US-11-079-463-5285	Sequence 5285, App
151	32	40.5	348	7	US-11-045-004-2586	Sequence 2586, App	224	31	39.2	226	7	US-11-096-568A-29157	Sequence 29157, A
152	32	40.5	362	7	US-11-109-157A-8	Sequence 8, Appl	225	31	39.2	229	7	US-11-079-463-7985	Sequence 7985, App
153	32	40.5	362	7	US-11-072-512-2732	Sequence 2732, App	226	31	39.2	236	7	US-11-054-281-118	Sequence 118, App
154	32	40.5	370	7	US-11-109-157A-41	Sequence 41, Appl	227	31	39.2	237	6	US-10-510-386-34	Sequence 34, Appl
155	32	40.5	376	6	US-11-072-512-2623	Sequence 2623, App	228	31	39.2	248	7	US-11-096-568A-29278	Sequence 29278, A
156	32	40.5	387	6	US-10-501-035-213	Sequence 213, App	229	31	39.2	255	7	US-11-096-568A-29125	Sequence 29125, A
157	32	40.5	394	6	US-10-821-234-1194	Sequence 1194, App	230	31	39.2	269	7	US-11-055-822-282	Sequence 282, App
158	32	40.5	414	7	US-11-096-568A-14688	Sequence 14688, A	231	31	39.2	269	7	US-11-055-822-618	Sequence 618, App
159	32	40.5	427	7	US-11-096-568A-14687	Sequence 14687, A	232	31	39.2	271	7	US-11-055-822-280	Sequence 280, App
160	32	40.5	434	6	US-10-915-003-216	Sequence 216, Appl	233	31	39.2	271	7	US-11-055-822-616	Sequence 616, App
161	32	40.5	437	6	US-10-850-465-2	Sequence 2, Appl	234	31	39.2	282	7	US-11-087-099-6624	Sequence 6624, App
162	32	40.5	441	7	US-11-087-099-10304	Sequence 10304, A	235	31	39.2	289	7	US-11-096-568A-29156	Sequence 29156, A
163	32	40.5	441	7	US-11-087-099-11270	Sequence 11270, A	236	31	39.2	289	7	US-11-087-099-8567	Sequence 8567, App
164	32	40.5	446	7	US-11-096-568A-27457	Sequence 27457, A	237	31	39.2	293	7	US-11-116-939-10	Sequence 10, Appl
165	32	40.5	451	7	US-11-096-568A-1960	Sequence 1960, App	238	31	39.2	293	7	US-11-098-686-10616	Sequence 10616, A
166	32	40.5	454	7	US-11-096-568A-27456	Sequence 27456, A	239	31	39.2	304	7	US-11-096-568A-29277	Sequence 29277, A
167	32	40.5	459	7	US-11-087-099-1361	Sequence 1361, App	240	31	39.2	311	7	US-11-096-568A-29124	Sequence 29124, A
168	32	40.5	464	7	US-11-172-740-2137	Sequence 2137, App	241	31	39.2	312	7	US-11-054-281-32	Sequence 32, Appl
169	32	40.5	468	7	US-11-188-298-14237	Sequence 14237, App	242	31	39.2	312	7	US-11-054-281-320	Sequence 320, App
170	32	40.5	475	7	US-11-096-568A-27455	Sequence 27455, A	243	31	39.2	312	7	US-11-054-281-324	Sequence 324, App
171	32	40.5	485	7	US-11-188-298-10345	Sequence 10345, A	244	31	39.2	320	7	US-11-072-512-2822	Sequence 2822, App
												US-11-096-568A-29155	Sequence 29155, A

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246	31	39.2	336	5	US-09-995-493-230	Sequence 230, Appl	319	30	38.0	18	7	US-11-145-861-173	Sequence 173, App
247	31	39.2	336	7	US-11-096-568A-33747	Sequence 33747, A	320	30	38.0	33	6	US-10-895-064-1334	Sequence 1334, Ap
248	31	39.2	342	7	US-11-096-568A-29276	Sequence 29276, A	321	30	38.0	33	6	US-11-129-741-1334	Sequence 1334, Ap
249	31	39.2	342	7	US-11-096-568A-33746	Sequence 33746, A	322	30	38.0	39	6	US-10-467-657-1510	Sequence 1510, Ap
250	31	39.2	343	7	US-11-096-568A-33745	Sequence 33745, A	323	30	38.0	64	6	US-10-467-657-632	Sequence 632, App
251	31	39.2	346	7	US-11-079-463-9218	Sequence 9218, A	324	30	38.0	64	6	US-10-475-075-790	Sequence 790, App
252	31	39.2	349	7	US-11-096-568A-29123	Sequence 29123, A	325	30	38.0	76	7	US-11-172-571-28	Sequence 28, Appl
253	31	39.2	357	7	US-11-188-298-486	Sequence 486, App	326	30	38.0	100	7	US-11-045-004-2684	Sequence 2684, Ap
254	31	39.2	386	7	US-11-096-568A-26027	Sequence 26027, A	327	30	38.0	119	7	US-11-097-812-72	Sequence 72, Appl
255	31	39.2	388	7	US-11-096-568A-26026	Sequence 26026, A	328	30	38.0	119	7	US-11-097-812-81	Sequence 81, Appl
256	31	39.2	389	6	US-10-513-118-2	Sequence 2, Appli	329	30	38.0	135	6	US-10-330-773-528	Sequence 528, App
257	31	39.2	391	7	US-11-087-099-4808	Sequence 4808, Ap	330	30	38.0	145	6	US-10-330-773-530	Sequence 530, App
258	31	39.2	392	7	US-11-087-099-8324	Sequence 8324, Ap	331	30	38.0	163	7	US-11-188-298-11871	Sequence 11871, A
259	31	39.2	399	6	US-10-853-533-3	Sequence 3, Appli	332	30	38.0	167	7	US-11-234-786-481	Sequence 481, App
260	31	39.2	403	6	US-10-983-011-2	Sequence 2, Appli	333	30	38.0	168	6	US-10-821-234-1426	Sequence 1426, Ap
261	31	39.2	403	7	US-11-109-156-29	Sequence 29, Appl	334	30	38.0	174	6	US-10-991-285-874	Sequence 874, App
262	31	39.2	409	6	US-10-467-657-4220	Sequence 4220, Ap	335	30	38.0	176	6	US-10-330-773-525	Sequence 525, App
263	31	39.2	409	6	US-10-467-657-7088	Sequence 7088, Ap	336	30	38.0	179	7	US-11-079-463-6974	Sequence 6974, Ap
264	31	39.2	409	7	US-11-188-298-3056	Sequence 3056, Ap	337	30	38.0	186	7	US-11-087-099-3432	Sequence 3432, Ap
265	31	39.2	409	7	US-11-188-298-18383	Sequence 18383, A	338	30	38.0	192	7	US-11-087-099-9855	Sequence 9855, Ap
266	31	39.2	412	7	US-11-116-939-12	Sequence 12, Appl	339	30	38.0	192	7	US-11-087-099-11223	Sequence 11223, A
267	31	39.2	412	7	US-11-188-298-574	Sequence 574, App	340	30	38.0	196	7	US-11-172-740-2035	Sequence 2035, Ap
268	31	39.2	420	7	US-11-188-298-10248	Sequence 10248, A	341	30	38.0	205	7	US-11-087-099-2318	Sequence 2318, Ap
269	31	39.2	421	7	US-11-188-298-7320	Sequence 7320, Ap	342	30	38.0	221	7	US-11-170-653-20	Sequence 20, Appl
270	31	39.2	423	6	US-10-853-533-2	Sequence 2, Appli	343	30	38.0	221	7	US-11-087-099-2693	Sequence 2693, Ap
271	31	39.2	423	7	US-11-008-570-30	Sequence 30, Appl	344	30	38.0	222	7	US-11-045-004-2607	Sequence 2607, Ap
272	31	39.2	437	7	US-11-096-568A-26025	Sequence 26025, A	345	30	38.0	227	7	US-11-170-653-21	Sequence 21, Appl
273	31	39.2	445	7	US-11-072-512-2209	Sequence 2209, Ap	346	30	38.0	227	7	US-11-170-653-22	Sequence 22, Appl
274	31	39.2	449	7	US-11-188-298-14638	Sequence 14638, A	347	30	38.0	243	7	US-11-188-298-8625	Sequence 8625, Ap
275	31	39.2	459	7	US-11-188-298-18157	Sequence 18157, A	348	30	38.0	244	7	US-11-188-298-6364	Sequence 6364, Ap
276	31	39.2	469	7	US-11-188-298-15973	Sequence 15973, A	349	30	38.0	245	7	US-11-087-099-8114	Sequence 8114, Ap
277	31	39.2	472	7	US-11-188-298-8005	Sequence 8005, Ap	350	30	38.0	247	6	US-10-467-657-7320	Sequence 7320, Ap
278	31	39.2	472	7	US-11-188-298-20912	Sequence 20912, A	351	30	38.0	249	7	US-11-172-740-2235	Sequence 2235, Ap
279	31	39.2	478	7	US-11-188-298-17361	Sequence 17361, A	352	30	38.0	250	6	US-10-793-626-2310	Sequence 2310, Ap
280	31	39.2	487	7	US-11-188-298-3772	Sequence 3772, Ap	353	30	38.0	266	7	US-11-234-786-534	Sequence 534, App
281	31	39.2	488	7	US-11-188-298-6013	Sequence 6013, Ap	354	30	38.0	273	6	US-10-793-626-608	Sequence 608, App
282	31	39.2	504	7	US-11-188-298-14675	Sequence 14675, A	355	30	38.0	274	7	US-11-188-298-17507	Sequence 17507, A
283	31	39.2	507	7	US-11-033-039-96	Sequence 96, Appl	356	30	38.0	274	7	US-11-188-298-19272	Sequence 19272, A
284	31	39.2	510	7	US-11-188-298-5258	Sequence 5258, Ap	357	30	38.0	282	7	US-11-183-205-40	Sequence 40, Appl
285	31	39.2	516	7	US-11-188-298-17942	Sequence 17942, A	358	30	38.0	288	7	US-11-087-099-11574	Sequence 11574, A
286	31	39.2	517	7	US-11-188-298-2805	Sequence 2805, Ap	359	30	38.0	293	7	US-11-096-568A-10770	Sequence 10770, A
287	31	39.2	518	7	US-11-188-298-20809	Sequence 20809, A	360	30	38.0	296	7	US-11-087-099-1580	Sequence 1580, Ap
288	31	39.2	525	7	US-11-188-298-3625	Sequence 3625, Ap	361	30	38.0	299	7	US-11-087-099-1439	Sequence 1439, Ap
289	31	39.2	546	7	US-11-188-298-16801	Sequence 16801, A	362	30	38.0	299	7	US-11-087-099-9542	Sequence 9542, Ap
290	31	39.2	552	6	US-10-467-657-4142	Sequence 4142, Ap	363	30	38.0	300	7	US-11-087-099-1528	Sequence 1528, Ap
291	31	39.2	558	6	US-10-506-454-972	Sequence 972, App	364	30	38.0	308	7	US-11-188-298-15926	Sequence 15926, A
292	31	39.2	580	7	US-11-045-004-2746	Sequence 2746, Ap	365	30	38.0	308	7	US-11-188-298-20337	Sequence 20337, A
293	31	39.2	659	6	US-10-793-626-1596	Sequence 1596, Ap	366	30	38.0	314	7	US-11-096-568A-2465	Sequence 2465, Ap
294	31	39.2	671	7	US-11-096-568A-28178	Sequence 28178, A	367	30	38.0	317	6	US-10-873-528-65	Sequence 65, Appl
295	31	39.2	672	7	US-11-096-568A-28177	Sequence 28177, A	368	30	38.0	326	7	US-11-087-099-731	Sequence 731, App
296	31	39.2	704	7	US-11-232-440-49	Sequence 49, Appl	369	30	38.0	326	7	US-11-087-099-2404	Sequence 2404, Ap
297	31	39.2	715	7	US-11-096-568A-28176	Sequence 28176, A	370	30	38.0	326	7	US-11-087-099-9532	Sequence 9532, Ap
298	31	39.2	746	7	US-11-072-175-169	Sequence 169, App	371	30	38.0	327	7	US-11-087-099-10124	Sequence 10124, A
299	31	39.2	824	7	US-11-116-933-11	Sequence 11, Appl	372	30	38.0	327	7	US-11-045-004-2672	Sequence 2672, Ap
300	31	39.2	1144	6	US-10-467-657-1820	Sequence 1820, Ap	373	30	38.0	328	7	US-11-087-099-4727	Sequence 4727, Ap
301	31	39.2	1190	7	US-11-043-889-20	Sequence 20, Appl	374	30	38.0	328	7	US-11-087-099-7553	Sequence 7553, Ap
302	31	39.2	1212	6	US-10-501-035-374	Sequence 374, App	375	30	38.0	329	7	US-11-087-099-1058	Sequence 1058, Ap
303	31	39.2	3748	7	US-11-132-686-8	Sequence 8, Appli	376	30	38.0	329	7	US-11-087-099-6155	Sequence 6155, Ap
304	31	39.2	3749	7	US-11-132-686-6	Sequence 6, Appli	377	30	38.0	329	7	US-11-087-099-9296	Sequence 9296, Ap
305	31	39.2	3749	7	US-11-132-686-12	Sequence 12, Appl	378	30	38.0	329	7	US-11-087-099-11934	Sequence 11934, A
306	31	39.2	3912	7	US-11-132-686-7	Sequence 7, Appli	379	30	38.0	330	7	US-11-087-099-6398	Sequence 6398, Ap
307	31	39.2	3913	7	US-11-132-686-5	Sequence 5, Appli	380	30	38.0	330	7	US-11-087-099-9899	Sequence 9899, Ap
308	31	39.2	3913	7	US-11-132-686-9	Sequence 9, Appli	381	30	38.0	334	7	US-11-087-099-7131	Sequence 7131, Ap
309	30.5	38.6	89	7	US-11-079-463-6577	Sequence 6577, Ap	382	30	38.0	345	7	US-11-188-298-13763	Sequence 13763, A
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311	30.5	38.6	210	7	US-11-096-568A-33330	Sequence 33330, A	384	30	38.0	349	7	US-11-096-568A-2464	Sequence 2464, Ap
312	30.5	38.6	233	7	US-11-096-568A-33329	Sequence 33329, A	385	30	38.0	365	7	US-11-072-512-3375	Sequence 3375, Ap
313	30.5	38.6	296	7	US-11-078-280-2	Sequence 2, Appli	386	30	38.0	375	6	US-10-469-469-115	Sequence 115, App
314	30.5	38.6	299	6	US-10-194-487-164	Sequence 164, App	387	30	38.0	378	7	US-11-087-099-12205	Sequence 12205, A
315	30.5	38.6	299	6	US-10-195-883-164	Sequence 164, App	388	30	38.0	380	7	US-11-150-845-44	Sequence 44, Appl
316	30.5	38.6	299	6	US-10-195-888-164	Sequence 164, App	389	30	38.0	380	7	US-11-150-487-38	Sequence 38, Appl
317	30.5	38.6	299	6	US-10-195-889-164	Sequence 164, App	390	30	38.0	387	7	US-11-010-795-5	Sequence 5, Appl
318	30.5	38.6	299	6	US-10-195-889-164	Sequence 164, App	390	30	38.0	387	7	US-11-010-795-14	Sequence 14, Appl

391	30	38.0	387	7	US-11-010-795-18	Sequence 18, Appl	464	29.5	37.3	186	6	US-10-667-295-166	Sequence 166, App
392	30	38.0	390	7	US-11-188-298-7867	Sequence 7867, Ap	465	29.5	37.3	186	6	US-10-667-295-199	Sequence 199, App
393	30	38.0	411	7	US-11-188-298-1737	Sequence 1737, Ap	466	29.5	37.3	186	7	US-11-172-740-2097	Sequence 2097, Ap
394	30	38.0	414	7	US-11-087-099-2837	Sequence 2837, Ap	467	29.5	37.3	199	7	US-11-045-004-1026	Sequence 1026, Ap
395	30	38.0	429	7	US-11-188-298-12329	Sequence 12329, A	468	29.5	37.3	204	6	US-10-667-295-165	Sequence 165, App
396	30	38.0	432	7	US-11-188-298-5835	Sequence 5835, Ap	469	29.5	37.3	204	6	US-10-667-295-198	Sequence 198, App
397	30	38.0	454	7	US-11-089-551A-35	Sequence 35, Appl	470	29.5	37.3	204	6	US-11-172-740-2092	Sequence 2092, Ap
398	30	38.0	456	7	US-11-188-298-2769	Sequence 2769, Ap	471	29.5	37.3	204	7	US-11-172-740-2093	Sequence 2093, Ap
399	30	38.0	490	7	US-11-096-568A-31601	Sequence 31601, A	472	29.5	37.3	204	7	US-11-172-740-2094	Sequence 2094, Ap
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401	30	38.0	492	7	US-11-188-298-18524	Sequence 18524, A	474	29.5	37.3	204	7	US-11-172-740-2096	Sequence 2096, Ap
402	30	38.0	496	7	US-11-096-568A-31600	Sequence 31600, A	475	29.5	37.3	204	7	US-11-172-740-2098	Sequence 2098, Ap
403	30	38.0	497	7	US-11-188-298-9664	Sequence 9664, Ap	476	29.5	37.3	227	6	US-10-667-295-197	Sequence 197, App
404	30	38.0	499	7	US-11-096-568A-15796	Sequence 15796, A	477	29.5	37.3	298	7	US-11-096-568A-3265	Sequence 3265, Ap
405	30	38.0	510	7	US-11-031-206-80	Sequence 80, Appl	478	29.5	37.3	298	7	US-11-096-568A-3266	Sequence 3266, Ap
406	30	38.0	517	7	US-11-098-686-11247	Sequence 11247, A	479	29.5	37.3	303	7	US-11-096-568A-3264	Sequence 3264, Ap
407	30	38.0	517	7	US-11-096-568A-15795	Sequence 15795, A	480	29.5	37.3	307	7	US-11-096-568A-3263	Sequence 3263, Ap
408	30	38.0	534	7	US-11-096-568A-31599	Sequence 31599, A	481	29.5	37.3	307	7	US-11-045-004-2693	Sequence 2693, Ap
409	30	38.0	559	6	US-10-521-162-4	Sequence 4, Appl	482	29.5	37.3	396	7	US-11-087-099-544	Sequence 544, App
410	30	38.0	560	6	US-10-995-561-1026	Sequence 1026, Ap	483	29.5	37.3	482	7	US-11-232-440-33	Sequence 33, Appl
411	30	38.0	566	7	US-11-188-298-6791	Sequence 6791, Ap	484	29.5	37.3	974	6	US-10-330-773-944	Sequence 944, App
412	30	38.0	566	7	US-11-188-298-22197	Sequence 22197, A	485	29.5	37.3	1164	7	US-11-087-099-2278	Sequence 2278, Ap
413	30	38.0	580	7	US-11-143-984A-30	Sequence 30, Appl	486	29.5	37.3	1164	7	US-11-087-099-9070	Sequence 9070, Ap
414	30	38.0	584	7	US-11-072-175-157	Sequence 157, App	487	29	36.7	25	7	US-11-083-624-44	Sequence 44, Appl
415	30	38.0	614	7	US-11-150-845-34	Sequence 34, Appl	488	29	36.7	25	7	US-11-223-699A-42	Sequence 42, Appl
416	30	38.0	614	7	US-11-150-487-34	Sequence 34, Appl	489	29	36.7	25	7	US-11-121-566A-42	Sequence 42, Appl
417	30	38.0	616	6	US-10-995-561-1018	Sequence 1018, Ap	490	29	36.7	35	7	US-11-083-624-55	Sequence 55, Appl
418	30	38.0	616	6	US-10-995-561-1022	Sequence 1022, Ap	491	29	36.7	35	7	US-11-037-199-46	Sequence 46, Appl
419	30	38.0	617	7	US-11-150-845-46	Sequence 46, Appl	492	29	36.7	35	7	US-11-004-399-3152	Sequence 3152, Ap
420	30	38.0	617	7	US-11-150-487-40	Sequence 40, Appl	493	29	36.7	53	6	US-10-914-391A-7	Sequence 7, Appl
421	30	38.0	638	7	US-11-087-099-1176	Sequence 1176, Ap	494	29	36.7	53	6	US-11-086-568A-3415	Sequence 3415, Ap
422	30	38.0	688	7	US-11-098-686-10191	Sequence 10191, A	495	29	36.7	82	6	US-10-467-657-564	Sequence 564, App
423	30	38.0	690	6	US-10-131-826A-306	Sequence 306, App	496	29	36.7	82	6	US-10-821-234-1505	Sequence 1505, Ap
424	30	38.0	690	6	US-10-973-115B-306	Sequence 306, App	497	29	36.7	92	6	US-10-763-712A-51	Sequence 51, Appl
425	30	38.0	690	7	US-11-290-153-306	Sequence 306, App	498	29	36.7	114	6	US-11-188-298-22057	Sequence 22057, A
426	30	38.0	702	6	US-10-467-657-7230	Sequence 7230, Ap	499	29	36.7	121	7	US-11-188-298-22057	Sequence 47, Appl
427	30	38.0	706	6	US-11-188-298-11914	Sequence 11914, A	500	29	36.7	137	6	US-10-527-500-47	Sequence 67, Appl
428	30	38.0	707	7	US-11-045-004-1281	Sequence 1281, Ap	501	29	36.7	145	7	US-11-088-570-62	Sequence 570, Appl
429	30	38.0	712	6	US-10-521-162-12	Sequence 12, Appl	502	29	36.7	157	6	US-10-467-657-5496	Sequence 5496, Ap
430	30	38.0	732	6	US-10-518-599-22	Sequence 22, Appl	503	29	36.7	161	7	US-11-087-099-10533	Sequence 10533, A
431	30	38.0	732	6	US-10-518-599-23	Sequence 23, Appl	504	29	36.7	162	7	US-11-106-270-8	Sequence 8, Appl
432	30	38.0	732	6	US-10-995-561-1020	Sequence 1020, Ap	505	29	36.7	196	6	US-10-467-657-7254	Sequence 7254, Ap
433	30	38.0	738	7	US-11-188-298-2319	Sequence 2319, Ap	506	29	36.7	196	6	US-10-467-657-8130	Sequence 8130, Ap
434	30	38.0	757	6	US-10-491-468-6	Sequence 6, Appl	507	29	36.7	197	7	US-11-087-099-5815	Sequence 5815, Ap
435	30	38.0	777	7	US-11-087-099-5818	Sequence 5818, Ap	508	29	36.7	201	7	US-11-156-516-27	Sequence 27, Appl
436	30	38.0	798	7	US-11-188-298-9773	Sequence 9773, Ap	509	29	36.7	204	7	US-11-169-041-161	Sequence 161, App
437	30	38.0	804	7	US-11-070-080-18	Sequence 18, Appl	510	29	36.7	211	7	US-11-116-943-2	Sequence 2, Appl
438	30	38.0	817	7	US-11-098-686-11041	Sequence 11041, A	511	29	36.7	217	7	US-11-045-004-497	Sequence 497, App
439	30	38.0	820	6	US-10-467-657-4910	Sequence 4910, Ap	512	29	36.7	226	7	US-11-024-559-501	Sequence 501, App
440	30	38.0	827	7	US-11-079-463-5603	Sequence 5603, Ap	513	29	36.7	226	7	US-11-072-512-2138	Sequence 2138, Ap
441	30	38.0	883	7	US-11-045-004-1556	Sequence 1556, Ap	514	29	36.7	229	7	US-11-045-004-1183	Sequence 1183, Ap
442	30	38.0	884	7	US-11-232-440-45	Sequence 45, Appl	515	29	36.7	240	7	US-11-232-440-29	Sequence 29, Appl
443	30	38.0	900	7	US-11-087-099-3766	Sequence 3766, Ap	516	29	36.7	253	7	US-11-054-515-860	Sequence 860, App
444	30	38.0	907	7	US-11-103-957-82	Sequence 82, Appl	517	29	36.7	253	7	US-11-096-568A-7429	Sequence 7429, Ap
445	30	38.0	912	6	US-10-467-657-7142	Sequence 7142, Ap	518	29	36.7	253	7	US-11-266-444-860	Sequence 860, App
446	30	38.0	915	7	US-11-087-099-6117	Sequence 6117, Ap	519	29	36.7	256	7	US-11-079-463-8557	Sequence 8557, App
447	30	38.0	920	7	US-11-087-099-11404	Sequence 11404, A	520	29	36.7	256	7	US-11-045-004-858	Sequence 858, App
448	30	38.0	920	7	US-11-188-298-21540	Sequence 21540, A	521	29	36.7	257	6	US-10-667-295-61	Sequence 61, Appl
449	30	38.0	932	7	US-11-079-463-6029	Sequence 6029, Ap	522	29	36.7	261	7	US-11-083-624-2	Sequence 2, Appl
450	30	38.0	937	7	US-11-079-463-7544	Sequence 7544, Ap	523	29	36.7	262	7	US-11-087-099-7815	Sequence 7815, Ap
451	30	38.0	965	7	US-11-079-463-5326	Sequence 5326, Ap	524	29	36.7	262	7	US-11-087-099-10891	Sequence 10891, A
452	30	38.0	1037	7	US-11-087-099-6333	Sequence 6333, Ap	525	29	36.7	262	7	US-11-172-740-1331	Sequence 1331, A
453	30	38.0	1100	7	US-11-045-004-2825	Sequence 2825, Ap	526	29	36.7	262	7	US-11-188-298-14411	Sequence 14411, A
454	30	38.0	1160	6	US-10-995-561-1019	Sequence 1019, Ap	527	29	36.7	271	7	US-11-195-739-3	Sequence 3, Appl
455	30	38.0	1302	6	US-10-995-561-1024	Sequence 1024, Ap	528	29	36.7	271	7	US-11-195-739-4	Sequence 4, Appl
456	30	38.0	1306	6	US-10-995-561-1027	Sequence 1027, Ap	529	29	36.7	275	7	US-11-087-099-5099	Sequence 5099, Ap
457	30	38.0	1375	6	US-10-995-561-809	Sequence 809, App	530	29	36.7	277	7	US-11-172-740-2183	Sequence 2183, Ap
458	30	38.0	1376	7	US-11-100-640-32	Sequence 32, Appl	531	29	36.7	283	7	US-11-188-298-14922	Sequence 14922, A
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461	30	38.0	1757	7	US-11-096-568A-32049	Sequence 32049, A	534	29	36.7	286	7	US-11-172-740-2262	Sequence 2262, Ap
462	29.5	37.3	150	6	US-11-067-295-162	Sequence 162, App	535	29	36.7	288	7	US-11-045-004-1259	Sequence 1259, Ap
463	29.5	37.3	168	6	US-10-667-295-161	Sequence 161, App	536	29	36.7	289	7	US-11-096-568A-32768	Sequence 32768, A

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539	29	36.7	296	7	US-11-045-004-629	Sequence 629, App	612	29	36.7	422	7	US-11-188-298-19174	Sequence 19174, A
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542	29	36.7	301	7	US-11-172-740-1326	Sequence 1326, App	615	29	36.7	430	6	US-10-467-657-5700	Sequence 5700, App
543	29	36.7	304	6	US-10-793-626-650	Sequence 650, App	616	29	36.7	431	7	US-11-096-568A-23163	Sequence 23163, App
544	29	36.7	306	6	US-10-793-626-1716	Sequence 1716, App	617	29	36.7	433	7	US-11-188-298-11844	Sequence 11844, A
545	29	36.7	306	6	US-10-330-773-901	Sequence 901, App	618	29	36.7	442	6	US-10-793-626-1000	Sequence 1000, App
546	29	36.7	306	7	US-11-188-298-13263	Sequence 12363, A	619	29	36.7	450	7	US-11-188-298-9452	Sequence 9452, App
547	29	36.7	312	7	US-11-096-568A-32766	Sequence 32766, A	620	29	36.7	451	6	US-10-506-454-691	Sequence 691, App
548	29	36.7	312	7	US-11-045-004-1285	Sequence 1285, App	621	29	36.7	452	7	US-11-188-298-8497	Sequence 8497, App
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554	29	36.7	327	6	US-10-667-295-59	Sequence 59, Appl	627	29	36.7	472	7	US-11-087-099-9252	Sequence 9252, App
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557	29	36.7	343	7	US-11-079-463-6346	Sequence 6346, App	630	29	36.7	472	7	US-11-188-298-21080	Sequence 21080, App
558	29	36.7	345	7	US-11-072-512-3023	Sequence 3023, App	631	29	36.7	474	7	US-11-188-298-19751	Sequence 19751, A
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560	29	36.7	354	7	US-11-096-568A-2990	Sequence 2990, App	633	29	36.7	484	7	US-11-096-568A-7428	Sequence 7428, App
561	29	36.7	360	7	US-11-172-740-1330	Sequence 1330, App	634	29	36.7	484	7	US-11-188-298-22333	Sequence 22333, A
562	29	36.7	360	7	US-11-188-298-13249	Sequence 13249, A	635	29	36.7	485	7	US-11-172-740-2136	Sequence 2136, App
563	29	36.7	363	7	US-11-087-099-5458	Sequence 5458, App	636	29	36.7	485	7	US-11-188-298-313	Sequence 313, App
564	29	36.7	363	7	US-11-188-298-22281	Sequence 22281, A	637	29	36.7	487	7	US-11-188-298-6934	Sequence 6934, App
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571	29	36.7	372	7	US-11-188-298-19827	Sequence 19827, A	644	29	36.7	522	6	US-10-467-657-7238	Sequence 7238, App
572	29	36.7	373	7	US-11-096-568A-23079	Sequence 23079, A	645	29	36.7	523	7	US-11-055-822-954	Sequence 954, App
573	29	36.7	373	7	US-11-096-568A-23165	Sequence 23165, A	646	29	36.7	535	7	US-11-188-298-13691	Sequence 13691, A
574	29	36.7	375	7	US-11-188-298-4639	Sequence 4639, App	647	29	36.7	537	7	US-11-098-686-11361	Sequence 11361, A
575	29	36.7	375	7	US-11-188-298-20720	Sequence 20720, A	648	29	36.7	549	7	US-11-194-246-431	Sequence 431, App
576	29	36.7	378	7	US-11-172-740-1329	Sequence 1329, App	649	29	36.7	550	7	US-11-113-837-17	Sequence 17, Appl
577	29	36.7	378	7	US-11-172-740-1335	Sequence 1335, App	650	29	36.7	554	7	US-11-000-463-240	Sequence 240, App
578	29	36.7	378	7	US-11-188-298-6856	Sequence 6856, App	651	29	36.7	563	6	US-10-878-556A-135	Sequence 135, App
579	29	36.7	378	7	US-11-188-298-15858	Sequence 15858, A	652	29	36.7	563	7	US-11-072-175-241	Sequence 241, App
580	29	36.7	379	7	US-11-096-568A-2989	Sequence 2989, App	653	29	36.7	585	7	US-11-188-298-6291	Sequence 6291, App
581	29	36.7	379	7	US-11-096-568A-2991	Sequence 2991, App	654	29	36.7	588	7	US-11-072-512-3053	Sequence 3053, App
582	29	36.7	380	6	US-10-204-639-39	Sequence 39, Appl	655	29	36.7	588	7	US-11-074-176-258	Sequence 258, App
583	29	36.7	382	7	US-11-096-568A-16256	Sequence 16256, A	656	29	36.7	607	7	US-11-188-298-13814	Sequence 13814, A
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586	29	36.7	384	7	US-11-096-568A-33730	Sequence 33730, A	659	29	36.7	624	7	US-11-073-463-10187	Sequence 10187, A
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591	29	36.7	392	7	US-11-188-298-19545	Sequence 19545, A	664	29	36.7	685	7	US-11-096-568A-33956	Sequence 33956, A
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593	29	36.7	393	7	US-11-188-298-10324	Sequence 10324, A	666	29	36.7	717	7	US-11-096-568A-33955	Sequence 33955, A
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595	29	36.7	395	7	US-11-188-298-10115	Sequence 10115, A	668	29	36.7	725	7	US-11-073-463-8952	Sequence 8952, App
596	29	36.7	396	7	US-11-096-568A-19736	Sequence 19736, A	669	29	36.7	740	7	US-11-079-463-8625	Sequence 8625, App
597	29	36.7	396	7	US-11-096-568A-31930	Sequence 31930, A	670	29	36.7	762	6	US-10-330-773-898	Sequence 898, App
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603	29	36.7	407	7	US-11-188-298-464	Sequence 464, App	676	29	36.7	842	7	US-11-045-004-2517	Sequence 2517, App
604	29	36.7	409	7	US-11-219-282-33	Sequence 33, Appl	677	29	36.7	856	7	US-11-073-463-5325	Sequence 5325, App
605	29	36.7	409	7	US-11-096-568A-19735	Sequence 19735, A	678	29	36.7	865	7	US-11-087-099-1496	Sequence 1496, App
606	29	36.7	409	7	US-11-188-298-12421	Sequence 12421, A	679	29	36.7	914	7	US-11-087-099-6835	Sequence 6835, App
607	29	36.7	409	7	US-11-188-298-15630	Sequence 15630, A	680	29	36.7	916	6	US-10-467-657-5232	Sequence 5232, App
608	29	36.7	411	6	US-10-467-657-5868	Sequence 5868, App	681	29	36.7	921	6	US-10-467-657-7354	Sequence 7354, App
609	29	36.7	415	7	US-11-087-099-1187	Sequence 1187, App	682	29	36.7	929	7	US-11-087-099-6648	Sequence 6648, App

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685	29	36.7	954	7	US-11-096-568A-31293	Sequence 31293, A	758	28	35.4	183	7	US-11-045-004-820	Sequence 820, App
686	29	36.7	963	6	US-10-467-962B-2	Sequence 2, Appli	759	28	35.4	189	6	US-10-873-528-15	Sequence 15, Appl
687	29	36.7	963	7	US-11-096-568A-31292	Sequence 31292, A	760	28	35.4	189	6	US-11-096-568A-3488	Sequence 3488, Ap
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690	29	36.7	1114	6	US-10-857-780-27	Sequence 27, Appl	763	28	35.4	193	6	US-10-537-897-33	Sequence 33, Appl
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692	29	36.7	1274	6	US-10-454-437-360	Sequence 360, App	765	28	35.4	204	6	US-10-467-657-8687	Sequence 8687, Ap
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694	29	36.7	1367	6	US-10-995-561-538	Sequence 538, App	767	28	35.4	209	7	US-11-188-298-4191	Sequence 4191, Ap
695	29	36.7	1367	6	US-10-510-903-10	Sequence 10, Appl	768	28	35.4	214	6	US-10-793-626-3124	Sequence 3124, Ap
696	29	36.7	1367	6	US-11-113-202-18	Sequence 18, Appl	769	28	35.4	216	7	US-11-096-568A-15125	Sequence 15125, A
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698	29	36.7	1394	7	US-11-096-568A-33411	Sequence 33411, A	771	28	35.4	221	6	US-10-921-286B-18	Sequence 18, Appl
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704	28.5	36.1	320	6	US-10-965-103-36	Sequence 36, Appl	777	28	35.4	227	7	US-11-188-298-13693	Sequence 13693, A
705	28.5	36.1	442	7	US-11-087-099-1764	Sequence 1764, Ap	778	28	35.4	227	7	US-11-188-298-20592	Sequence 20592, A
706	28.5	36.1	442	7	US-11-188-298-1756	Sequence 1756, Ap	779	28	35.4	228	7	US-11-104-111-8	Sequence 8, Appli
707	28.5	36.1	487	6	US-10-131-826A-528	Sequence 528, App	780	28	35.4	228	7	US-11-188-298-1688	Sequence 1688, Ap
708	28.5	36.1	487	6	US-10-973-115B-528	Sequence 528, App	781	28	35.4	228	7	US-11-188-298-21739	Sequence 21739, A
709	28.5	36.1	487	6	US-10-213-535-18	Sequence 18, Appl	782	28	35.4	229	6	US-10-923-327-14	Sequence 14, Appl
710	28.5	36.1	487	6	US-10-218-784-204	Sequence 204, App	783	28	35.4	231	7	US-11-072-512-3576	Sequence 3576, Ap
711	28.5	36.1	487	6	US-10-219-061-204	Sequence 204, App	784	28	35.4	231	7	US-11-188-298-19681	Sequence 19681, A
712	28.5	36.1	487	6	US-10-219-062-204	Sequence 204, App	785	28	35.4	233	6	US-10-923-327-19	Sequence 19, Appl
713	28.5	36.1	487	6	US-10-219-064-204	Sequence 204, App	786	28	35.4	233	7	US-11-072-512-3056	Sequence 3056, Ap
714	28.5	36.1	487	6	US-10-233-134-204	Sequence 204, App	787	28	35.4	233	7	US-11-096-568A-15123	Sequence 15123, A
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ALIGNMENTS

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; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
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; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
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; TITLE OF INVENTION: Genetic Polymorphisms Associated with
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; SEQ ID NO 215
; LENGTH: 2668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-215
```

```
Query Match 100.0%; Score 79; DB 7; Length 2668;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQRRSSRS 15
Db 189 RHYGETKNQRRSSRS 203
```

```
RESULT 3
US-11-096-568A-32400
; Sequence 32400, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32400
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(726)
; OTHER INFORMATION: Ceres Seq. ID no. 13592891
US-11-096-568A-32400
```

```
Query Match 64.6%; Score 51; DB 7; Length 726;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 RHYGETKNQRRSSRS 15
Db 106 RKIGETSLNRRSSRS 120
```

```
RESULT 4
US-11-096-568A-28686
; Sequence 28686, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28686
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
```

; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(743)
US-11-096-568A-28686

Query Match 64.6%; Score 51; DB 7; Length 743;
Best Local Similarity 66.7%; Pred. No. 0.33;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 86 RKIGETSLNRSRS 100

RESULT 5

US-11-096-568A-32399
; Sequence 32399, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32399
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(829)
; OTHER INFORMATION: Ceres Seq. ID no. 13592890
US-11-096-568A-32399

Query Match 64.6%; Score 51; DB 7; Length 829;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 209 RKIGETSLNRSRS 223

RESULT 6

US-11-096-568A-32398
; Sequence 32398, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32398
; LENGTH: 834
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(834)
; OTHER INFORMATION: Ceres Seq. ID no. 13592889
US-11-096-568A-32398

Query Match 64.6%; Score 51; DB 7; Length 834;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15

Db 214 RKIGETSLNRSRS 228
| | | | | : | : | | | | |

RESULT 7

US-11-096-568A-28685
; Sequence 28685, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28685
; LENGTH: 851
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(851)
; OTHER INFORMATION: Ceres Seq. ID no. 3036348
US-11-096-568A-28685

Query Match 64.6%; Score 51; DB 7; Length 851;
Best Local Similarity 66.7%; Pred. No. 0.38;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 194 RKIGETSLNRSRS 208

RESULT 8

US-11-096-568A-28684
; Sequence 28684, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28684
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(862)
; OTHER INFORMATION: Ceres Seq. ID no. 3036347
US-11-096-568A-28684

Query Match 64.6%; Score 51; DB 7; Length 862;
Best Local Similarity 66.7%; Pred. No. 0.38;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRSRS 15
| | | | | : | : | | | | |
Db 205 RKIGETSLNRSRS 219

RESULT 9

US-11-096-568A-29848
; Sequence 29848, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

```
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29846
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(811)
; OTHER INFORMATION: Ceres Seq. ID no. 4931842
US-11-096-568A-29846

Query Match      58.2%; Score 46; DB 7; Length 811;
Best Local Similarity 60.0%; Pred. No. 2.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMQRSRS 15
Db      86 RQVGETALNDKSSRS 100

RESULT 10
US-11-096-568A-29847
; Sequence 29847, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29847
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(898)
; OTHER INFORMATION: Ceres Seq. ID no. 4931841
US-11-096-568A-29847

Query Match      58.2%; Score 46; DB 7; Length 898;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMQRSRS 15
Db      173 RQVGETALNDKSSRS 187

RESULT 11
US-11-096-568A-29846
; Sequence 29846, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29846
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)..(932)
; OTHER INFORMATION: Ceres Seq. ID no. 4931840
US-11-096-568A-29846

Query Match      58.2%; Score 46; DB 7; Length 932;
Best Local Similarity 60.0%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1 RHYGETKMQRSRS 15
Db      207 RQVGETALNDKSSRS 221

RESULT 12
US-11-045-004-555
; Sequence 555, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALLE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOBBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNIA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 555
```

```
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-555

Query Match      57.0%; Score 45; DB 7; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 RHYGETKNQRS 12
      || ||| ||| |||
Db      201 RHAGETKNYRS 212

RESULT 13
US-11-051-720-1349
; Sequence 1349, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1349
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1349

Query Match      57.0%; Score 45; DB 7; Length 324;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 14
US-11-051-720-1348
; Sequence 1348, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1348
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1348

Query Match      57.0%; Score 45; DB 7; Length 385;
Best Local Similarity 60.0%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 15
US-11-051-720-1346
; Sequence 1346, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1346
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1346

Query Match      57.0%; Score 45; DB 7; Length 514;
Best Local Similarity 60.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 16
US-11-051-720-1345
; Sequence 1345, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1345
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1345

Query Match      57.0%; Score 45; DB 7; Length 737;
Best Local Similarity 60.0%; Pred. No. 3.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
      || ||| ||| |||
Db      191 RHVAVTNMNEHSRS 205

RESULT 17
US-10-330-773-712
; Sequence 712, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773-712

Query Match      57.0%; Score 45; DB 6; Length 911;
Best Local Similarity 60.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
```

```
Db      149 RHVAVTNNEHSRS 163
||      ||      ||      ||      ||
RESULT 18
US-10-330-773-709
; Sequence 709, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 709
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-330-773-709

Query Match      57.0%; Score 45; DB 6; Length 952;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
||      ||      ||      ||      ||
Db      191 RHVAVTNNEHSRS 205

RESULT 19
US-11-051-720-1438
; Sequence 1438, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1438
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1438

Query Match      57.0%; Score 45; DB 7; Length 957;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
||      ||      ||      ||      ||
Db      191 RHVAVTNNEHSRS 205

RESULT 20
US-11-096-568A-26779
; Sequence 26779, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26779
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-096-568A-26779

Query Match      55.7%; Score 44; DB 7; Length 338;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(292)
; OTHER INFORMATION: Ceres Seq. ID no. 13600527
US-11-096-568A-26779

Query Match      55.7%; Score 44; DB 7; Length 292;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
||      ||      ||      ||      ||
Db      8 RAVGSTALNERSRS 22

RESULT 21
US-11-096-568A-26778
; Sequence 26778, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26778
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(331)
; OTHER INFORMATION: Ceres Seq. ID no. 13600526
US-11-096-568A-26778

Query Match      55.7%; Score 44; DB 7; Length 331;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQSRSS 15
||      ||      ||      ||      ||
Db      47 RAVGSTALNERSRS 61

RESULT 22
US-11-096-568A-26777
; Sequence 26777, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26777
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(338)
; OTHER INFORMATION: Ceres Seq. ID no. 13600525
US-11-096-568A-26777

Query Match      55.7%; Score 44; DB 7; Length 338;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 RHYGETKNQRSRS 15
Db      54 RAVGSTALNERSRS 68

RESULT 23
US-11-096-568A-26771
; Sequence 26771, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26771
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(799)
; OTHER INFORMATION: Ceres Seq. ID no. 13600313
US-11-096-568A-26771

Query Match      55.7%; Score 44; DB 7; Length 799;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
Db      470 RAVGSTALNERSRS 484

RESULT 24
US-11-096-568A-26949
; Sequence 26949, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26949
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(808)
; OTHER INFORMATION: Ceres Seq. ID no. 13635666
US-11-096-568A-26949

Query Match      55.7%; Score 44; DB 7; Length 808;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
Db      86 RRTGETYLNERSRS 100

RESULT 25
US-11-096-568A-26770
; Sequence 26770, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26770
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(842)
; OTHER INFORMATION: Ceres Seq. ID no. 13600312
US-11-096-568A-26770

Query Match      55.7%; Score 44; DB 7; Length 842;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
Db      513 RAVGSTALNERSRS 527

RESULT 26
US-11-096-568A-26769
; Sequence 26769, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26769
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(849)
; OTHER INFORMATION: Ceres Seq. ID no. 13600311
US-11-096-568A-26769

Query Match      55.7%; Score 44; DB 7; Length 849;
Best Local Similarity 60.0%; Pred. No. 6.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RHYGETKNQRSRS 15
Db      520 RAVGSTALNERSRS 534

RESULT 27
US-11-096-568A-26948
; Sequence 26948, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26948
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
```

;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(897)
; OTHER INFORMATION: Ceres Seq. ID no. 13635665
US-11-096-568A-26948

Query Match 55.7%; Score 44; DB 7; Length 897;
Best Local Similarity 60.0%; Pred. No. 7.2;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 175 RRTGETYLNSSRS 189

RESULT 28
US-11-096-568A-27943
; Sequence 27943, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27943
; LENGTH: 975
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(975)
; OTHER INFORMATION: Ceres Seq. ID no. 2142331
US-11-096-568A-27943

Query Match 54.4%; Score 43; DB 7; Length 975;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 78 RKIGETSLNEVSSRS 92

RESULT 29
US-11-096-568A-27942
; Sequence 27942, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27942
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(983)
; OTHER INFORMATION: Ceres Seq. ID no. 2142330
US-11-096-568A-27942

Query Match 54.4%; Score 43; DB 7; Length 983;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 78 RKIGETSLNEVSSRS 92

RESULT 30
US-11-096-568A-30324
; Sequence 30324, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30324
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(1039)
; OTHER INFORMATION: Ceres Seq. ID no. 4953855
US-11-096-568A-30324

Query Match 54.4%; Score 43; DB 7; Length 1039;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 177 RQIGETALNEVSSRS 191

RESULT 31
US-11-096-568A-30323
; Sequence 30323, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30323
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)..(1055)
; OTHER INFORMATION: Ceres Seq. ID no. 4953854
US-11-096-568A-30323

Query Match 54.4%; Score 43; DB 7; Length 1055;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQRRSSRS 15
| ||| :|: ||||
Db 193 RQIGETALNEVSSRS 207

RESULT 32
US-11-096-568A-30322
; Sequence 30322, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30322
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1063)
; OTHER INFORMATION: Ceres Seq. ID no. 4953853
US-11-096-568A-30322

Query Match 54.4%; Score 43; DB 7; Length 1063;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | | |
Db 201 RQIGETALNEVSSRS 215

RESULT 33
US-11-096-568A-27941
; Sequence 27941, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27941
; LENGTH: 1087
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1087)
; OTHER INFORMATION: Ceres Seq. ID no. 2142329
US-11-096-568A-27941

Query Match 54.4%; Score 43; DB 7; Length 1087;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | | |
Db 190 RKIGETSLNEVSSRS 204

RESULT 34
US-11-096-568A-34153
; Sequence 34153, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34153
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)..(970)
; OTHER INFORMATION: Ceres Seq. ID no. 13605257
US-11-096-568A-34153

Query Match 51.9%; Score 41; DB 7; Length 970;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | | |
Db 151 RATGSTNNNQSRSS 165

RESULT 35
US-11-096-568A-34152
; Sequence 34152, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34152
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1035)
; OTHER INFORMATION: Ceres Seq. ID no. 13605256
US-11-096-568A-34152

Query Match 51.9%; Score 41; DB 7; Length 1035;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | | |
Db 216 RATGSTNNNQSRSS 230

RESULT 36
US-11-096-568A-34151
; Sequence 34151, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34151
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1042)
; OTHER INFORMATION: Ceres Seq. ID no. 13605255
US-11-096-568A-34151

Query Match 51.9%; Score 41; DB 7; Length 1042;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RHYGETKNQSRSS 15
| | | | | : | | | | |
Db 223 RATGSTNNNQSRSS 237

```
RESULT 37
US-11-082-389-84
; Sequence 84, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 84
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-84

Query Match          50.6%; Score 40; DB 7; Length 302;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
      |||||
DB 287 RHYGETVSGSEKAS 301

RESULT 38
US-11-087-099-3831
; Sequence 3831, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3831
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-087-099-3831

Query Match          50.6%; Score 40; DB 7; Length 1142;
```

```
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YGETKNQRSRS 15
      :|||:|||||
DB 485 FSTTKNKRSSRS 497

RESULT 39
US-11-079-463-10327
; Sequence 10327, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10327
; LENGTH: 453
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-10327

Query Match          48.1%; Score 38; DB 7; Length 453;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HYGETKNQR 11
      ||:|||||
DB 15 HYSKTSMNKR 24

RESULT 40
US-11-188-298-19543
; Sequence 19543, Application US/11188298
; Publication No. US2006007522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19543
; LENGTH: 506
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-19543

Query Match          48.1%; Score 38; DB 7; Length 506;
Best Local Similarity 57.1%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HYGETKNQRSRS 15
      :|||:|||||
DB 466 HAEKQLNARSRS 479

RESULT 41
US-10-506-454-292
; Sequence 292, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
```

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; APPLICANT: Mezheva, Katja V
; APPLICANT: Poluehin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 292
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-292

Query Match          46.8%; Score 37; DB 6; Length 290;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETK 7
DB 50 RHYGETE 56

RESULT 42
US-11-098-686-11287
; Sequence 11287, Application US/11098686
; Publication No. US2006002496A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11287
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11287

Query Match          46.8%; Score 37; DB 7; Length 334;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 3 YGETKNQRRSR 14
DB 33 FGQTKMNSGTR 44

RESULT 43
US-11-098-686-10227
; Sequence 10227, Application US/11098686
; Publication No. US2006002496A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
```

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; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10227
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10227

Query Match          46.8%; Score 37; DB 7; Length 353;
Best Local Similarity 53.8%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HYGETKNQRRSR 14
DB 231 HYGETLSQLPSR 243

RESULT 44
US-11-087-099-422
; Sequence 422, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 422
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-087-099-422

Query Match          46.8%; Score 37; DB 7; Length 575;
Best Local Similarity 57.1%; Pred. No. 83;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 HYGETKNQRRSR 15
DB 415 HMLETRQSRSSSS 428

RESULT 45
US-11-096-568A-29274
; Sequence 29274, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29274
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1145)
; OTHER INFORMATION: Ceres Seq. ID no. 4805154
US-11-096-568A-29274

Query Match          46.8%; Score 37; DB 7; Length 1145;
```

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; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNICK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAGRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045.004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1154
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1154

Query Match 45.6%; Score 36; DB 7; Length 204;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 HYGETKNQRS 12
DB 65 YYGKEKNQES 75

RESULT 49
US-11-188-298-20356

; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29273
; LENGTH: 1160
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1160)
; OTHER INFORMATION: Ceres Seq. ID no. 4805153
US-11-096-568A-29273

Query Match 46.8%; Score 37; DB 7; Length 1160;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
DB 647 RAVGKTTANEHSRS 661

RESULT 47
US-11-096-568A-29272
; Sequence 29272, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29272
; LENGTH: 1195
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1195)
; OTHER INFORMATION: Ceres Seq. ID no. 4805152
US-11-096-568A-29272

Query Match 46.8%; Score 37; DB 7; Length 1195;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RHYGETKNQRSRS 15
DB 682 RAVGKTTANEHSRS 696

RESULT 48
US-11-045-004-1154
; Sequence 1154, Application US/11045004
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; Sequence 20356, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20356
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Cicer arietinum
US-11-188-298-20356

Query Match 45.6%; Score 36; DB 7; Length 313;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 RHYGETKMNQR 11
Db 64 RHY--SKMNQR 72

RESULT 50
US-11-152-569-12
; Sequence 12, Application US/11152569
; Publication No. US20060005278A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Nehring, Ramla
; APPLICANT: McGrath, Robert B.
; TITLE OF INVENTION: ETHYLENE INSENSITIVE PLANTS
; FILE REFERENCE: 532792001210
; CURRENT APPLICATION NUMBER: US/11/152,569
; CURRENT FILING DATE: 2005-06-13
; PRIOR APPLICATION NUMBER: 10/144,156
; PRIOR FILING DATE: 2002-10-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-11-152-569-12

Query Match 45.6%; Score 36; DB 7; Length 317;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RHYGETKM 8
Db 179 QHYGDTKL 186

Search completed: April 21, 2006, 13:57:21
Job time : 34 secs

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